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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Goodman, Corey S.
Kidd, Thomas
Mitchell, Kevin
Tear, Guy
- (ii) TITLE OF INVENTION: Robo: A Novel Family of Polypeptide and Nucleic Acids
- (iii) NUMBER OF SEQUENCES: 13
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
(B) STREET: 75 DENISE DRIVE
(C) CITY: HILLSBOROUGH
(D) STATE: CALIFORNIA
(E) COUNTRY: USA
(F) ZIP: 94010
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: OSMAN, RICHARD A
(B) REGISTRATION NUMBER: 36,627
(C) REFERENCE/DOCKET NUMBER: B98-006
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (650) 343-4341
(B) TELEFAX: (650) 343-4342

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGCATCCCA	TGCATCCCGA	AAACCACGCC	ATCGCCCGGA	GCACGAGCAC	CACTAATAAC	60
CCATCTCGCA	GTCGGAGCAG	CAGGATGTGG	CTCCTGCCCG	CCTGGCTGCT	CCTCGTCCTG	120
GTGGCCAGCA	ATGGCCTGCC	AGCAGTCAGA	GGCCAGTACC	AATCGCCACG	TATCATCGAG	180
CATCCCACGG	ATCTGGTCGT	TAAGAAGAAT	GAACCCGCCA	CGCTCAACTG	CAAAGTGGAG	240
GGCAAGCCGG	AACCCACCAT	TGAGTGGTTT	AAGGATGGCG	AACCCGTCAG	CACCAACGAA	300
AAGAAATCGC	ACCGCGTCCA	GTTCAAGGAC	GGCGCCCTCT	TCTTTTACAG	GACAATGCAA	360
GGCAAGAAGG	AGCAGGACGG	CGGAGAGTAC	TGGTGCGTGG	CCAAGAACCG	AGTGGGCCAG	420
GCCGTTAGTC	GCCATGCCTC	CCTCCAGATA	GCTGTTTTGC	GCGACGATTT	TCGCGTGGAG	480
CCCAAAGACA	CGCGAGTGGC	CAAAGGCGAG	ACGGCTCTGC	TGGAGTGTGG	GCCGCCCAAA	540
GGCATTCCAG	AGCCAACGCT	GATTTGGATA	AAGGACGGCG	TTCCCTTGGA	CGACCTGAAA	600
GCCATGTCGT	TTGGCGCCAG	CTCCCGCGTT	CGAATTGTGG	ACGGTGGCAA	CCTGCTGATC	660
AGCAATGTGG	AGCCCATTTGA	TGAGGGCAAC	TACAAGTGCA	TTGCCAGAA	TCTGGTAGGC	720
ACCCGCGAGA	GCAGCTATGC	CAAGCTGATT	GTCCAGGTCA	AACCATACTT	TATGAAGGAG	780

CCCAAGGATC	AGGTGATGCT	CTACGGCCAG	ACAGCCACTT	TCCACTGCTC	AGTGGGCGGT	840
GATCCGCCGC	CGAAAGTGTT	GTGGAAAAAG	GAGGAGGGCA	ATATTCCGGT	GTCCAGAGCG	900
CGAATCCTTC	ACGACGAGAA	AAGTTTAGAG	ATATCCAACA	TAACGCCCCAC	CGATGAGGGC	960
ACCTATGTCT	GCGAGGCACA	CAACAATGTC	GGTCAGATCA	GCGCTAGGGC	TTCTCTTATA	1020
GTCCACGCTC	CGCCGAACCT	TACGAAAAGA	CCCAGTAACA	AGAAAAGTGGG	ACTAAATGGG	1080
GTTGTCCAAC	TACCTTGCAT	GGCCTCCGGA	AACCCTCCGC	CGTCTGTATT	CTGGACCAAG	1140
GAAGGAGTAT	CCACTCTTAT	GTTCCCAAAT	AGTTCGCACG	GAAGGCAGTA	TGTGGCTGCC	1200
GATGGAACTC	TGCAGATTAC	GGATGTGCGG	CAGGAAGACG	AAGGCTACTA	TGTGTGTTCC	1260
GCTTTCAGTG	TAGTCGATTG	CTCTACAGTA	CGGGTTTTTC	TGCAAGTCAG	CTCGGTAGAC	1320
GAGCGTCCAC	CTCCGATTAT	TCAAATCGGA	CCTGCCAATC	AAACACTGCC	CAAGGGATCA	1380
GTTGCTACTT	TACCCTGTCT	GGCCACTGGA	AATCCCAGTC	CCCGTATCAA	GTGGTTCCAC	1440
GATGGACATG	CCGTACAAGC	GGGCAATCGA	TACAGCATCA	TCCAAGGAAG	CTCACTGAGA	1500
GTCGATGACC	TTCAACTAAG	TGACTCTGGT	ACCTACACCT	GCACTGCATC	TGGCGAACGA	1560
GGAGAACTT	CCTGGGCTGC	CACACTAACG	GTGGAAAAAC	CCGGTTCTAC	ATCTCTTCAC	1620
CGGGCAGCTG	ATCCTAGCAC	TTATCCTGCT	CCTCCAGGAA	CACCTAAAGT	CCTGAATGTC	1680
AGTCGCACCA	GCATTAGTCT	TCGTTGGGCT	AAAAGCCAAG	AGAAACCCGG	AGCTGTGGGC	1740
CCAATCATTG	GATACACTGT	AGAGTACTTC	AGTCCGGATC	TGCAAACCTGG	TTGGATTGTG	1800
GCTGCCCATC	GAGTCGGCGA	CACTCAAGTC	ACTATCTCGG	GTCTCACTCC	TGGCACTTCG	1860
TATGTGTTCC	TAGTTAGAGC	TGAGAATACT	CAGGGTATTT	CTGTGCCTTC	CGGCTTATCA	1920
AATGTTATTA	AAACCATTTGA	GGCAGATTTT	GATGCAGCTT	CTGCCAATGA	TTTGTCAGCA	1980
GCTCGAACTT	TGCTGACAGG	AAAGTCGGTG	GAGCTAATAG	ATGCCTCGGC	TATCAATGCT	2040
AGTGCCGTTA	GACTTGAGTG	GATGCTCCAC	GTGAGCGCTG	ATGAGAAATA	CGTAGAGGGC	2100
CTGCGCATAC	ACTATAAGGA	TGCCAGTGTA	CCATCCGCAC	AGTATCACTC	GATCACTGTT	2160
ATGGATGCCT	CTGCAGAATC	GTTTGTGGTG	GGAAACCTTA	AGAAGTACAC	CAAGTATGAG	2220
TTCTTCCTAA	CACCCTTTTT	TGAGACAATT	GAAGGACAGC	CCAGTAACTC	CAAGACAGCC	2280
CTCACCTATG	AAGATGTTCC	CTCCGCACCA	CCGGATAACA	TTCAGATTGG	CATGTACAAC	2340
CAAACAGCCG	GTTGGGTGCG	TTGGACTCCG	CCACCCTCCC	AGCACCACAA	TGGCAATTTG	2400
TATGGCTACA	AGATTGAGGT	CAGCGCCGGT	AACACCATGA	AGGTGCTGGC	CAATATGACT	2460
CTTAATGCTA	CCACCACATC	TGTGCTCCTA	AATAACCTAA	CCACCGGAGC	TGTGTACAGC	2520
GTGAGGTTGA	ACTCCTTTAC	CAAGGCAGGA	GATGGACCTT	ACTCCAAACC	GATATCACTA	2580
TTCATGGACC	CCACCCATCA	TGTGCATCCG	CCACGGGCAC	ATCCAAGCGG	CACCCATGAT	2640
GGGCGACATG	AGGGACAGGA	TCTCACGTAT	CATAACAATG	GCAACATACC	ACCTGGCGAC	2700
ATTAATCCCA	CCACTCATAA	AAAGACCACT	GACTACCTAT	CTGGACCGTG	GCTAATGGTG	2760
CTGGTCTGCA	TCGTCTTTCT	AGTCCTGGTT	ATTTCCGGCG	CTATTTTCGAT	GGTCTACTTC	2820
AAGCGCAAGC	ATCAAATGAC	CAAGGAATTG	GGTCACTTAA	GTGTGGTCAG	TGACAACGAA	2880
ATAACCGCAT	TAAATATCAA	TAGCAAAGAG	AGCCTTTGGA	TAGACCATCA	TCGTGGATGG	2940
CGAACTGCCG	ATACTGACAA	AGACTCAGGA	TTAAGCGAAT	CGAAGCTACT	ATCCCACGTT	3000
AACAGCAGTC	AATCCAACCTA	CAATAACTCC	GATGGAGGAA	CCGATTATGC	AGAAGTTGAC	3060
ACCCGTAACC	TTACCACCTT	CTACAATTGT	CGCAAGAGCC	CCGATAATCC	CACGCCGTAC	3120
GCCACCACTA	TGATCATTGG	TACCTCTTCC	AGTGAGACCT	GCACCAAGAC	AACATCTATA	3180
AGTGCCGATA	AGGACTCGGG	AACTCATTCG	CCCTATTCTG	ACGCATTTCG	CGGTCAGGTG	3240
CCAGCGGTTT	CTGTTGTCAA	ATCCAACCTAT	CTTCAGTATC	CGGTTGAACC	GATCAACTGG	3300
TCAGAGTTTC	TACCCCCGCC	GCCAGAACAC	CCACCTCCGT	CTTCTACCTA	TGGATACGCA	3360
CAAGGATCTC	CTGAATCTTC	GCGGAAGAGC	TCCAAAAGCG	CAGGTTCCGG	CATTTCTACA	3420
AATCAAAGCA	TTCTGAACGC	ATCCATACAC	AGCAGCTCCT	CGGGCGGCTT	TTCAGCTTGG	3480
GGAGTATCGC	CCCAATATGC	TGTCGCCTGT	CCACCGGAAA	ACGTTTATAG	CAATCCGCTG	3540
TCGGCAGTGG	CTGGCGGCAC	CCAGAACCGC	TATCAGATAA	CGCCACAAA	CCAACATCCG	3600
CCACAGTTAC	CGGCCTACTT	TGCCACCACG	GGTCCAGGAG	GAGCTGTACC	ACCCAACCAC	3660
CTGCCATTTG	CCACACAGCG	TCATGCAGCC	AGCGAGTACC	AGGCTGGACT	GAATGCAGCG	3720
CGATGTGCCC	AAAGCCGCGC	CTGCAACAGC	TGCGATGCCT	TGGCCACACC	CTCGCCCATG	3780
CAACCCCCAC	CGCCAGTTCC	CGTACCCGAG	GGCTGGTACC	AACCGGTGCA	TCCCAATAGC	3840
CACCCGATGC	ACCCGACCTC	CTCCAACCAC	CAGATCTACC	AGTGCTCCTC	CGAGTGCTCG	3900
GATCACTCGA	GGAGCTCGCA	GAGTCACAAG	CGGCAGCTGC	AGCTCGAGGA	GCACGGCAGC	3960
AGTGCCAAAC	AACGCGGAGG	ACACCACCGT	CGACGAGCCC	CGGTGGTGCA	GCCGTGCATG	4020

GAGAGCGAGA	ACGAGAACAT	GCTGGCGGAG	TACGAGCAGC	GCCAGTACAC	CAGCGATTGC	4080
TGCAATAGCT	CCCGCGAGGG	CGACACCTGC	TCCTGCAGCG	AGGGATCCTG	TCTTTACGCC	4140
GAGGCGGGCG	AGCCGGCGCC	TCGTCAAATG	ACTGCTAAGA	ACACCTAA		4188

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1395 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	His	Pro	Met	His	Pro	Glu	Asn	His	Ala	Ile	Ala	Arg	Ser	Thr	Ser	1	5	10	15
Thr	Thr	Asn	Asn	Pro	Ser	Arg	Ser	Arg	Ser	Ser	Arg	Met	Trp	Leu	Leu	20	25	30	
Pro	Ala	Trp	Leu	Leu	Leu	Val	Leu	Val	Ala	Ser	Asn	Gly	Leu	Pro	Ala	35	40	45	
Val	Arg	Gly	Gln	Tyr	Gln	Ser	Pro	Arg	Ile	Ile	Glu	His	Pro	Thr	Asp	50	55	60	
Leu	Val	Val	Lys	Lys	Asn	Glu	Pro	Ala	Thr	Leu	Asn	Cys	Lys	Val	Glu	65	70	75	80
Gly	Lys	Pro	Glu	Pro	Thr	Ile	Glu	Trp	Phe	Lys	Asp	Gly	Glu	Pro	Val	85	90	95	
Ser	Thr	Asn	Glu	Lys	Lys	Ser	His	Arg	Val	Gln	Phe	Lys	Asp	Gly	Ala	100	105	110	
Leu	Phe	Phe	Tyr	Arg	Thr	Met	Gln	Gly	Lys	Lys	Glu	Gln	Asp	Gly	Gly	115	120	125	
Glu	Tyr	Trp	Cys	Val	Ala	Lys	Asn	Arg	Val	Gly	Gln	Ala	Val	Ser	Arg	130	135	140	
His	Ala	Ser	Leu	Gln	Ile	Ala	Val	Leu	Arg	Asp	Asp	Phe	Arg	Val	Glu	145	150	155	160
Pro	Lys	Asp	Thr	Arg	Val	Ala	Lys	Gly	Glu	Thr	Ala	Leu	Leu	Glu	Cys	165	170	175	
Gly	Pro	Pro	Lys	Gly	Ile	Pro	Glu	Pro	Thr	Leu	Ile	Trp	Ile	Lys	Asp	180	185	190	
Gly	Val	Pro	Leu	Asp	Asp	Leu	Lys	Ala	Met	Ser	Phe	Gly	Ala	Ser	Ser	195	200	205	
Arg	Val	Arg	Ile	Val	Asp	Gly	Gly	Asn	Leu	Leu	Ile	Ser	Asn	Val	Glu	210	215	220	
Pro	Ile	Asp	Glu	Gly	Asn	Tyr	Lys	Cys	Ile	Ala	Gln	Asn	Leu	Val	Gly	225	230	235	240
Thr	Arg	Glu	Ser	Ser	Tyr	Ala	Lys	Leu	Ile	Val	Gln	Val	Lys	Pro	Tyr	245	250	255	
Phe	Met	Lys	Glu	Pro	Lys	Asp	Gln	Val	Met	Leu	Tyr	Gly	Gln	Thr	Ala	260	265	270	
Thr	Phe	His	Cys	Ser	Val	Gly	Gly	Asp	Pro	Pro	Pro	Lys	Val	Leu	Trp	275	280	285	
Lys	Lys	Glu	Glu	Gly	Asn	Ile	Pro	Val	Ser	Arg	Ala	Arg	Ile	Leu	His	290	295	300	
Asp	Glu	Lys	Ser	Leu	Glu	Ile	Ser	Asn	Ile	Thr	Pro	Thr	Asp	Glu	Gly	305	310	315	320
Thr	Tyr	Val	Cys	Glu	Ala	His	Asn	Asn	Val	Gly	Gln	Ile	Ser	Ala	Arg	325	330	335	

Ala	Ser	Leu	Ile	Val	His	Ala	Pro	Pro	Asn	Phe	Thr	Lys	Arg	Pro	Ser			
			340					345					350					
Asn	Lys	Lys	Val	Gly	Leu	Asn	Gly	Val	Val	Gln	Leu	Pro	Cys	Met	Ala			
		355					360					365						
Ser	Gly	Asn	Pro	Pro	Pro	Ser	Val	Phe	Trp	Thr	Lys	Glu	Gly	Val	Ser			
	370					375					380							
Thr	Leu	Met	Phe	Pro	Asn	Ser	Ser	His	Gly	Arg	Gln	Tyr	Val	Ala	Ala			
385					390					395					400			
Asp	Gly	Thr	Leu	Gln	Ile	Thr	Asp	Val	Arg	Gln	Glu	Asp	Glu	Gly	Tyr			
				405					410					415				
Tyr	Val	Cys	Ser	Ala	Phe	Ser	Val	Val	Asp	Ser	Ser	Thr	Val	Arg	Val			
		420					425						430					
Phe	Leu	Gln	Val	Ser	Ser	Val	Asp	Glu	Arg	Pro	Pro	Pro	Ile	Ile	Gln			
	435						440					445						
Ile	Gly	Pro	Ala	Asn	Gln	Thr	Leu	Pro	Lys	Gly	Ser	Val	Ala	Thr	Leu			
450						455					460							
Pro	Cys	Arg	Ala	Thr	Gly	Asn	Pro	Ser	Pro	Arg	Ile	Lys	Trp	Phe	His			
465					470					475					480			
Asp	Gly	His	Ala	Val	Gln	Ala	Gly	Asn	Arg	Tyr	Ser	Ile	Ile	Gln	Gly			
				485					490					495				
Ser	Ser	Leu	Arg	Val	Asp	Asp	Leu	Gln	Leu	Ser	Asp	Ser	Gly	Thr	Tyr			
		500					505					510						
Thr	Cys	Thr	Ala	Ser	Gly	Glu	Arg	Gly	Glu	Thr	Ser	Trp	Ala	Ala	Thr			
	515						520					525						
Leu	Thr	Val	Glu	Lys	Pro	Gly	Ser	Thr	Ser	Leu	His	Arg	Ala	Ala	Asp			
530						535					540							
Pro	Ser	Thr	Tyr	Pro	Ala	Pro	Pro	Gly	Thr	Pro	Lys	Val	Leu	Asn	Val			
545					550					555					560			
Ser	Arg	Thr	Ser	Ile	Ser	Leu	Arg	Trp	Ala	Lys	Ser	Gln	Glu	Lys	Pro			
				565					570					575				
Gly	Ala	Val	Gly	Pro	Ile	Ile	Gly	Tyr	Thr	Val	Glu	Tyr	Phe	Ser	Pro			
		580					585						590					
Asp	Leu	Gln	Thr	Gly	Trp	Ile	Val	Ala	Ala	His	Arg	Val	Gly	Asp	Thr			
	595						600					605						
Gln	Val	Thr	Ile	Ser	Gly	Leu	Thr	Pro	Gly	Thr	Ser	Tyr	Val	Phe	Leu			
610						615						620						
Val	Arg	Ala	Glu	Asn	Thr	Gln	Gly	Ile	Ser	Val	Pro	Ser	Gly	Leu	Ser			
625					630					635					640			
Asn	Val	Ile	Lys	Thr	Ile	Glu	Ala	Asp	Phe	Asp	Ala	Ala	Ser	Ala	Asn			
				645					650					655				
Asp	Leu	Ser	Ala	Ala	Arg	Thr	Leu	Leu	Thr	Gly	Lys	Ser	Val	Glu	Leu			
		660					665						670					
Ile	Asp	Ala	Ser	Ala	Ile	Asn	Ala	Ser	Ala	Val	Arg	Leu	Glu	Trp	Met			
	675						680						685					
Leu	His	Val	Ser	Ala	Asp	Glu	Lys	Tyr	Val	Glu	Gly	Leu	Arg	Ile	His			
	690						695					700						
Tyr	Lys	Asp	Ala	Ser	Val	Pro	Ser	Ala	Gln	Tyr	His	Ser	Ile	Thr	Val			
705					710					715					720			
Met	Asp	Ala	Ser	Ala	Glu	Ser	Phe	Val	Val	Gly	Asn	Leu	Lys	Lys	Tyr			
				725					730					735				
Thr	Lys	Tyr	Glu	Phe	Phe	Leu	Thr	Pro	Phe	Phe	Glu	Thr	Ile	Glu	Gly			
		740					745						750					
Gln	Pro	Ser	Asn	Ser	Lys	Thr	Ala	Leu	Thr	Tyr	Glu	Asp	Val	Pro	Ser			
		755					760					765						

Ala	Pro	Pro	Asp	Asn	Ile	Gln	Ile	Gly	Met	Tyr	Asn	Gln	Thr	Ala	Gly	
770						775					780					
Trp	Val	Arg	Trp	Thr	Pro	Pro	Pro	Ser	Gln	His	His	Asn	Gly	Asn	Leu	
785					790					795					800	
Tyr	Gly	Tyr	Lys	Ile	Glu	Val	Ser	Ala	Gly	Asn	Thr	Met	Lys	Val	Leu	
			805						810					815		
Ala	Asn	Met	Thr	Leu	Asn	Ala	Thr	Thr	Thr	Ser	Val	Leu	Leu	Asn	Asn	
			820					825					830			
Leu	Thr	Thr	Gly	Ala	Val	Tyr	Ser	Val	Arg	Leu	Asn	Ser	Phe	Thr	Lys	
		835					840					845				
Ala	Gly	Asp	Gly	Pro	Tyr	Ser	Lys	Pro	Ile	Ser	Leu	Phe	Met	Asp	Pro	
850						855					860					
Thr	His	His	Val	His	Pro	Pro	Arg	Ala	His	Pro	Ser	Gly	Thr	His	Asp	
865					870					875					880	
Gly	Arg	His	Glu	Gly	Gln	Asp	Leu	Thr	Tyr	His	Asn	Asn	Gly	Asn	Ile	
			885						890					895		
Pro	Pro	Gly	Asp	Ile	Asn	Pro	Thr	Thr	His	Lys	Lys	Thr	Thr	Asp	Tyr	
			900					905					910			
Leu	Ser	Gly	Pro	Trp	Leu	Met	Val	Leu	Val	Cys	Ile	Val	Leu	Leu	Val	
		915				920						925				
Leu	Val	Ile	Ser	Ala	Ala	Ile	Ser	Met	Val	Tyr	Phe	Lys	Arg	Lys	His	
930						935					940					
Gln	Met	Thr	Lys	Glu	Leu	Gly	His	Leu	Ser	Val	Val	Ser	Asp	Asn	Glu	
945					950					955					960	
Ile	Thr	Ala	Leu	Asn	Ile	Asn	Ser	Lys	Glu	Ser	Leu	Trp	Ile	Asp	His	
			965						970					975		
His	Arg	Gly	Trp	Arg	Thr	Ala	Asp	Thr	Asp	Lys	Asp	Ser	Gly	Leu	Ser	
		980					985						990			
Glu	Ser	Lys	Leu	Leu	Ser	His	Val	Asn	Ser	Ser	Gln	Ser	Asn	Tyr	Asn	
		995				1000						1005				
Asn	Ser	Asp	Gly	Gly	Thr	Asp	Tyr	Ala	Glu	Val	Asp	Thr	Arg	Asn	Leu	
1010						1015					1020					
Thr	Thr	Phe	Tyr	Asn	Cys	Arg	Lys	Ser	Pro	Asp	Asn	Pro	Thr	Pro	Tyr	
1025					1030					1035					1040	
Ala	Thr	Thr	Met	Ile	Ile	Gly	Thr	Ser	Ser	Ser	Glu	Thr	Cys	Thr	Lys	
			1045						1050					1055		
Thr	Thr	Ser	Ile	Ser	Ala	Asp	Lys	Asp	Ser	Gly	Thr	His	Ser	Pro	Tyr	
		1060					1065					1070				
Ser	Asp	Ala	Phe	Ala	Gly	Gln	Val	Pro	Ala	Val	Pro	Val	Val	Lys	Ser	
		1075				1080						1085				
Asn	Tyr	Leu	Gln	Tyr	Pro	Val	Glu	Pro	Ile	Asn	Trp	Ser	Glu	Phe	Leu	
1090						1095					1100					
Pro	Pro	Pro	Pro	Glu	His	Pro	Pro	Pro	Ser	Ser	Thr	Tyr	Gly	Tyr	Ala	
1105					1110					1115					1120	
Gln	Gly	Ser	Pro	Glu	Ser	Ser	Arg	Lys	Ser	Ser	Lys	Ser	Ala	Gly	Ser	
			1125						1130					1135		
Gly	Ile	Ser	Thr	Asn	Gln	Ser	Ile	Leu	Asn	Ala	Ser	Ile	His	Ser	Ser	
		1140					1145					1150				
Ser	Ser	Gly	Gly	Phe	Ser	Ala	Trp	Gly	Val	Ser	Pro	Gln	Tyr	Ala	Val	
		1155				1160						1165				
Ala	Cys	Pro	Pro	Glu	Asn	Val	Tyr	Ser	Asn	Pro	Leu	Ser	Ala	Val	Ala	
	1170					1175					1180					
Gly	Gly	Thr	Gln	Asn	Arg	Tyr	Gln	Ile	Thr	Pro	Thr	Asn	Gln	His	Pro	
1185					1190					1195					1200	

Pro Gln Leu Pro Ala Tyr Phe Ala Thr Thr Gly Pro Gly Gly Ala Val
1205 1210 1215
Pro Pro Asn His Leu Pro Phe Ala Thr Gln Arg His Ala Ala Ser Glu
1220 1225 1230
Tyr Gln Ala Gly Leu Asn Ala Ala Arg Cys Ala Gln Ser Arg Ala Cys
1235 1240 1245
Asn Ser Cys Asp Ala Leu Ala Thr Pro Ser Pro Met Gln Pro Pro Pro
1250 1255 1260
Pro Val Pro Val Pro Glu Gly Trp Tyr Gln Pro Val His Pro Asn Ser
1265 1270 1275 1280
His Pro Met His Pro Thr Ser Ser Asn His Gln Ile Tyr Gln Cys Ser
1285 1290 1295
Ser Glu Cys Ser Asp His Ser Arg Ser Ser Gln Ser His Lys Arg Gln
1300 1305 1310
Leu Gln Leu Glu Glu His Gly Ser Ser Ala Lys Gln Arg Gly Gly His
1315 1320 1325
His Arg Arg Arg Ala Pro Val Val Gln Pro Cys Met Glu Ser Glu Asn
1330 1335 1340
Glu Asn Met Leu Ala Glu Tyr Glu Gln Arg Gln Tyr Thr Ser Asp Cys
1345 1350 1355 1360
Cys Asn Ser Ser Arg Glu Gly Asp Thr Cys Ser Cys Ser Glu Gly Ser
1365 1370 1375
Cys Leu Tyr Ala Glu Ala Gly Glu Pro Ala Pro Arg Gln Met Thr Ala
1380 1385 1390
Lys Asn Thr
1395

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGTGAATATC	CACGCATCAT	CGAGCATCCC	ATGGACACGA	CGGTGCCAAA	AAATGATCCA	60
TTTACGTTTA	ATTGCCAGGC	CGAGGGCAAT	CCAACACCAA	CCATTCAATG	GTTTAAGGAC	120
GGTCGCGAAC	TGAAGACGGA	TACGGGTTCG	CATCGCATAA	TGCTGCCCCG	CGGGGGTCTA	180
TTCTTTTCTCA	AGGTTATCCA	CTCACGTAGA	GAGAGCGATG	CGGGCACTTA	CTGGTGCGAG	240
GCCAAAAACG	AGTTTGAGT	GGCACGGTCC	AGGAATGCAA	CGTTGCAAGT	GGCAGTTCTC	300
CGCGACGAAT	TCCGTTTGGA	GCCGGCAAAT	ACCCGCGTGG	CCCAAGGCGA	GGTGGCCCTG	360
ATGGAATGCG	GTGCCCCCGG	AGGATCTCCG	GAGCCGCAAA	TCTCGTGGCG	CAAGAACGGC	420
CAGACCCTGA	ATCTTGTCGG	GAACAAGCGG	ATTTCGATTG	TCGACGGTGG	CAATCTGGCC	480
ATCCAGGAAG	CCCGCCAATC	GGACGACGGA	CGCTACCACT	GTGTGGTCAA	GAATGTGGTT	540
GGCACCCGGG	AGTCGGCCAC	CGCTTTTCTT	AAAGTGCATG	TACGTCCATT	CCTCATCCGA	600
GGACCCGAGA	ATCAGACGGC	GGTGGTGGGC	AGCTCGGTGG	TCTTCCAGTG	CCGCATCGGA	660
GGCGATCCCC	TGCTGATGT	CCTGTGGCGA	CGCACTGCCT	CCGGCGGCAA	TATGCCACTG	720
CGTAAGTTT	CTTGCTTCA	TTCAGCTTCA	GGTCGTGTGC	ACGTACTTGA	GGACCGCAGT	780
CTGAAGCTGG	ACGACGTTAC	TCTGGAGGAC	ATGGGCGAGT	ACACTTGCGA	GGCGGACAAT	840
GCGGTGGGCG	GCATCACGGC	CACTGGCATC	CTCACCGTTC	ACGCTCCCCC	CAAATTTGTG	900
ATACGCCCA	AGAATCAGCT	GGTGGAGATC	GGTGATGAAG	TGCTGTTCGA	GTGCCAAGCG	960
AATGGACATC	CCCGACCAAC	GCTCTACTGG	TCGGTGGAGG	GCAACAGCTC	CCTGCTGCTC	1020
CCCGGCTATC	GGGATGGCCG	CATGGAAGTG	ACCCTGACGC	CCGAGGGGCG	CTCGGTGCTC	1080
TCGATAGCTC	GATTTGCCCG	TGAGGATTCC	GGAAAGGTGG	TCACTTGCAA	CGCCCTGAAC	1140

GCCGTGGGCA	GCGTCAGCAG	TCGGACTGTG	GTCAGTGTGG	ATACGCAATT	CGAGCTGCCA	1200
CCGCCGATTA	TGAAACAGGG	GCCCGTGAAT	CAAACGTTGC	CCGTTAAATC	AATTGTGGTT	1260
CTGCCATGCC	GAAGCTCTGGG	CACTCCAGTG	CCACAGGTCT	CTTGGTACCT	GGATGGCATA	1320
CCCATCGATG	TGCAGGAGCA	CGAGCGGCGG	AATCTTTTCGG	ACGCTGGAGC	CTTAACCATT	1380
TCGGATCTTC	AGCGCCACGA	GGATGAAGGC	TTGTACACCT	GCGTGGCCAG	CAATCGCAAC	1440
GGAAAATCCT	CTTGGAGTGG	TTACCTTCGT	CTGGACACCC	CGACAAATCC	GAATATCAAG	1500
TTCTTCAGAG	CCCAGAACT	TTCCACCTAC	CCAGGGCCGC	CAGGAAAACC	GCAAATGGTG	1560
GAGAAGGGCG	AAAATTCGGT	GACTCTCAGC	TGGACGAGGA	GCAACAAGGT	GGGCGGCTCC	1620
AGTCTGGTGG	GCTATGTAAT	CGAGATGTTT	GGCAAAAACG	AAACGGATGG	CTGGGTGGCT	1680
GTGGGCACTA	GGGTGCAAAA	TACCACGTTT	ACCCAAACGG	GTCTGCTGCC	GGGTGTGAAT	1740
TACTTCTTTC	TAATTCGAGC	CGAGAACTCC	CATGGCTTAT	CACTGCCCAG	TCCGATGTCT	1800
GAACCCATTA	CGGTGGGAAC	GCGCTACTTC	AATAGTGGTC	TGGATCTGAG	CGAGGCTCGT	1860
GCCAGTCTGC	TGTCCGGAGA	TGTTGTGGAG	CTGAGCAACG	CCAGTGTGGT	GGACTCCACT	1920
AGCATGAAAC	TCACCTGGCA	GATCATCAAT	GGCAAATACG	TCGAGGGCTT	CTATGTCTAT	1980
GCGAGACAGT	TGCCAAATCC	AATAGTCAAC	AATCCGGCGC	CCGTTACTAG	CAATACCAAT	2040
CCGCTGCTGG	GCTCTACATC	CACATCCGCA	TCCGCATCCG	CCTCGGCATC	GGCATTGATT	2100
TCGACAAAGC	CAAAATATTG	AGCTGCCGGC	AAACGTGATG	GGGAGACAAA	CCAGAGTGGA	2160
GGAGGAGCTC	CGACCCCACT	GAACACCAAG	TATCGCATGC	TAACGATTCT	CAATGGCGGT	2220
GGCGCCTCAT	CCTGCACCAT	CACCGGGCTC	GTCCAGTACA	CGCTGTATGA	ATTTTTCATC	2280
GTGCCATTTT	ACAAATCCGT	CGAGGGCAAG	CCGTGCAATT	CGCGCATCGC	TCGCACCCTT	2340
GAAGATGTTT	CCTCTGAGGC	ACCATATGGA	ATGGAGGCTC	TGCTGTTGAA	CTCCTCCGCG	2400
GTCTTCTCTA	AATGGAAGGC	ACCAGAACTC	AAGGATCGGC	ATGGTGTCTT	CTTGAACAT	2460
CATGTTATAG	TCCGAGGTAT	TGACACTGCC	CACAATTTCT	CACGCATTTT	GACAAATGTC	2520
ACCATCGATG	CCGCTTCGCC	TACTCTGGTT	TTGGCCAATC	TCACCGAAGG	CGTCATGTAC	2580
ACCGTGGGCG	TGGCGGCCGG	AAATAACGCT	GGAGTTGGTC	CTTATTGTGT	CCCAGCTACT	2640
TTGCGTTTGG	ATCCCATCAC	AAAGCGACTC	GATCCGTTCA	TCAATCAGCG	GGACCATGTT	2700
AACGATGTGC	TGACGCAGCC	CTGGTTTATA	ATACTCCTGG	GCGCCATCCT	GGCCGTTCTT	2760
ATGCTGTCTT	TTGGCGCAAT	GGTCTTTGTG	AAGCGCAAGC	ACATGATGAT	GAAGCAGTCG	2820
GCCCTAAATA	CAATGCGTGG	CAATCACACG	AGCGACGTGC	TCAAAAATGCC	GAGTCTATCG	2880
GCGCGCAATG	GAAACGGCTA	CTGGCTGGAC	TCCTCCACCG	GCGGAATGGT	GTGGCGTCCC	2940
TCGCCCCGCG	GCGACTCGCT	GGAGATGCAA	AAGGATCACA	TCGCCGACTA	TGCGCCGGTC	3000
TGCGGTGCCC	CCGTTCTCTC	GGCCGGCGGT	GGCACCTCTT	CCGTTGGATC	CGGTGGCGCG	3060
GGCAGCGGTG	CCAGCGGCGG	CGATGACATT	CATGGAGGAC	ACGGCAGCGA	ACGCAATCAG	3120
CAGCGGTACG	TGGGCGAGTA	CTCCAACATA	CCGACCGACT	ATGCAGAGGT	GTCCAGTTTT	3180
GGCAAGGCAC	CCAGCGAGTA	TGGTCGGCAT	GGCAACGCCT	CCCCGGCCCC	TTATGCCACC	3240
TCTTCGATCC	TGAGTCCCCA	CCAGCAGCAA	CAGCAGCAGC	AGCCGCGTTA	TCAACAGCGA	3300
CCAGTGCCCG	GCTATGGGCT	CCAGCGCCCA	ATGCACCCAC	ACTACCAGCA	GCAGCAGCAT	3360
CAGCAGCAAC	AGGCGCAGCA	GACGCACCAG	CAACACCAGG	CTCTCCAGCA	GCACCAGCAA	3420
CTGCCACCCA	GCAACATCTA	CCAGCAGATG	TCCACCACCA	GCGAGATATA	CCCCACGAAC	3480
ACGGGTCTTT	CGCGCTCTGT	CTACTCTGAG	CAGTATTACT	ACCCCAAGGA	CAAGCAGAGA	3540
CACATCCACA	TCACCGAGAA	CAAGCTGAGC	AACTGCCACA	CCTATGAGGC	GGCTCCTGGC	3600
GCCAAGCAGT	CCTCGCCGAT	ATCCTCGCAG	TTCGCCAGCG	TGAGGCGGCA	GCAGCTGCCG	3660
CCCAACTGCA	GCATCGGCAG	GGAAAGTGCC	CGCTTCAAGG	TGCTAAACAC	GGATCAGGGC	3720
AAGAACCAGC	AGAATCTCCT	GGATCTCGAC	GGCTCCTCGA	TGTGCTACAA	CGGTCTGGCA	3780
GACTCGGGCT	GCGGTGGATC	TCCCTCCCCG	ATGGCCATGC	TGATGTCGCA	CGAGGACGAG	3840
CACGCGCTGT	ACCACACGGC	GGATGGGGAT	CTGGACGACA	TGGAACGACT	GTACGTCAAG	3900
GTGGACGAGC	AGCAGCCTCC	ACAGCAGCAG	CAGCAGCTGA	TTCCCCTGGT	CCCACAGCAT	3960
CCGGCGGAAG	GTCACCTGCA	GTCCTGGCGG	AATCAGAGCA	CGCGGAGCAG	TCGGAAGAAC	4020
GGCCAGGAAT	GCATCAAGGA	ACCCAGCGAG	TTGATCTACG	CTCCGGGAAG	CGTGGCCAGC	4080
GAACGGAGCC	TCCTCAGCAA	CTCGGGTAGC	GGCACCAGCA	GCCAGCCAGC	TGGCCACAAT	4140
GTCTGA						4146

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1381 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gly	Glu	Asn	Pro	Arg	Ile	Ile	Glu	His	Pro	Met	Asp	Thr	Thr	Val	Pro
1				5				10						15	
Lys	Asn	Asp	Pro	Phe	Thr	Phe	Asn	Cys	Gln	Ala	Glu	Gly	Asn	Pro	Thr
			20					25					30		
Pro	Thr	Ile	Gln	Trp	Phe	Lys	Asp	Gly	Arg	Glu	Leu	Lys	Thr	Asp	Thr
			35				40					45			
Gly	Ser	His	Arg	Ile	Met	Leu	Pro	Ala	Gly	Gly	Leu	Phe	Phe	Leu	Lys
						55					60				
Val	Ile	His	Ser	Arg	Arg	Glu	Ser	Asp	Ala	Gly	Thr	Tyr	Trp	Cys	Glu
65					70				75					80	
Ala	Lys	Asn	Glu	Phe	Gly	Val	Ala	Arg	Ser	Arg	Asn	Ala	Thr	Leu	Gln
				85				90						95	
Val	Ala	Val	Leu	Arg	Asp	Glu	Phe	Arg	Leu	Glu	Pro	Ala	Asn	Thr	Arg
			100					105					110		
Val	Ala	Gln	Gly	Glu	Val	Ala	Leu	Met	Glu	Cys	Gly	Ala	Pro	Arg	Gly
		115					120					125			
Ser	Pro	Glu	Pro	Gln	Ile	Ser	Trp	Arg	Lys	Asn	Gly	Gln	Thr	Leu	Asn
		130				135					140				
Leu	Val	Gly	Asn	Lys	Arg	Ile	Arg	Ile	Val	Asp	Gly	Gly	Asn	Leu	Ala
145					150					155				160	
Ile	Gln	Glu	Ala	Arg	Gln	Ser	Asp	Asp	Gly	Arg	Tyr	Gln	Cys	Val	Val
				165				170						175	
Lys	Asn	Val	Val	Gly	Thr	Arg	Glu	Ser	Ala	Thr	Ala	Phe	Leu	Lys	Val
			180					185					190		
His	Val	Arg	Pro	Phe	Leu	Ile	Arg	Gly	Pro	Gln	Asn	Gln	Thr	Ala	Val
		195				200						205			
Val	Gly	Ser	Ser	Val	Val	Phe	Gln	Cys	Arg	Ile	Gly	Gly	Asp	Pro	Leu
	210				215						220				
Pro	Asp	Val	Leu	Trp	Arg	Arg	Thr	Ala	Ser	Gly	Gly	Asn	Met	Pro	Leu
225					230					235				240	
Arg	Lys	Phe	Ser	Trp	Leu	His	Ser	Ala	Ser	Gly	Arg	Val	His	Val	Leu
			245					250						255	
Glu	Asp	Arg	Ser	Leu	Lys	Leu	Asp	Asp	Val	Thr	Leu	Glu	Asp	Met	Gly
			260				265						270		
Glu	Tyr	Thr	Cys	Glu	Ala	Asp	Asn	Ala	Val	Gly	Gly	Ile	Thr	Ala	Thr
		275				280						285			
Gly	Ile	Leu	Thr	Val	His	Ala	Pro	Pro	Lys	Phe	Val	Ile	Arg	Pro	Lys
	290					295					300				
Asn	Gln	Leu	Val	Glu	Ile	Gly	Asp	Glu	Val	Leu	Phe	Glu	Cys	Gln	Ala
305					310					315				320	
Asn	Gly	His	Pro	Arg	Pro	Thr	Leu	Tyr	Trp	Ser	Val	Glu	Gly	Asn	Ser
			325					330						335	
Ser	Leu	Leu	Leu	Pro	Gly	Tyr	Arg	Asp	Gly	Arg	Met	Glu	Val	Thr	Leu
			340				345						350		
Thr	Pro	Glu	Gly	Arg	Ser	Val	Leu	Ser	Ile	Ala	Arg	Phe	Ala	Arg	Glu
		355				360						365			
Asp	Ser	Gly	Lys	Val	Val	Thr	Cys	Asn	Ala	Leu	Asn	Ala	Val	Gly	Ser
	370					375					380				

Val	Ser	Ser	Arg	Thr	Val	Val	Ser	Val	Asp	Thr	Gln	Phe	Glu	Leu	Pro	385	390	395	400
Pro	Pro	Ile	Ile	Glu	Gln	Gly	Pro	Val	Asn	Gln	Thr	Leu	Pro	Val	Lys	405	410		415
Ser	Ile	Val	Val	Leu	Pro	Cys	Arg	Thr	Leu	Gly	Thr	Pro	Val	Pro	Gln	420	425		430
Val	Ser	Trp	Tyr	Leu	Asp	Gly	Ile	Pro	Ile	Asp	Val	Gln	Glu	His	Glu	435	440		445
Arg	Arg	Asn	Leu	Ser	Asp	Ala	Gly	Ala	Leu	Thr	Ile	Ser	Asp	Leu	Gln	450	455		460
Arg	His	Glu	Asp	Glu	Gly	Leu	Tyr	Thr	Cys	Val	Ala	Ser	Asn	Arg	Asn	465	470		475
Gly	Lys	Ser	Ser	Trp	Ser	Gly	Tyr	Leu	Arg	Leu	Asp	Thr	Pro	Thr	Asn	485	490		495
Pro	Asn	Ile	Lys	Phe	Phe	Arg	Ala	Pro	Glu	Leu	Ser	Thr	Tyr	Pro	Gly	500	505		510
Pro	Pro	Gly	Lys	Pro	Gln	Met	Val	Glu	Lys	Gly	Glu	Asn	Ser	Val	Thr	515	520		525
Leu	Ser	Trp	Thr	Arg	Ser	Asn	Lys	Val	Gly	Gly	Ser	Ser	Leu	Val	Gly	530	535		540
Tyr	Val	Ile	Glu	Met	Phe	Gly	Lys	Asn	Glu	Thr	Asp	Gly	Trp	Val	Ala	545	550		555
Val	Gly	Thr	Arg	Val	Gln	Asn	Thr	Thr	Phe	Thr	Gln	Thr	Gly	Leu	Leu	565	570		575
Pro	Gly	Val	Asn	Tyr	Phe	Phe	Leu	Ile	Arg	Ala	Glu	Asn	Ser	His	Gly	580	585		590
Leu	Ser	Leu	Pro	Ser	Pro	Met	Ser	Glu	Pro	Ile	Thr	Val	Gly	Thr	Arg	595	600		605
Tyr	Phe	Asn	Ser	Gly	Leu	Asp	Leu	Ser	Glu	Ala	Arg	Ala	Ser	Leu	Leu	610	615		620
Ser	Gly	Asp	Val	Val	Glu	Leu	Ser	Asn	Ala	Ser	Val	Val	Asp	Ser	Thr	625	630		635
Ser	Met	Lys	Leu	Thr	Trp	Gln	Ile	Ile	Asn	Gly	Lys	Tyr	Val	Glu	Gly	645	650		655
Phe	Tyr	Val	Tyr	Ala	Arg	Gln	Leu	Pro	Asn	Pro	Ile	Val	Asn	Asn	Pro	660	665		670
Ala	Pro	Val	Thr	Ser	Asn	Thr	Asn	Pro	Leu	Leu	Gly	Ser	Thr	Ser	Thr	675	680		685
Ser	Ala	Ser	Ala	Ser	Ala	Ser	Ala	Ser	Ala	Leu	Ile	Ser	Thr	Lys	Pro	690	695		700
Asn	Ile	Ala	Ala	Ala	Gly	Lys	Arg	Asp	Gly	Glu	Thr	Asn	Gln	Ser	Gly	705	710		715
Gly	Gly	Ala	Pro	Thr	Pro	Leu	Asn	Thr	Lys	Tyr	Arg	Met	Leu	Thr	Ile	725	730		735
Leu	Asn	Gly	Gly	Gly	Ala	Ser	Ser	Cys	Thr	Ile	Thr	Gly	Leu	Val	Gln	740	745		750
Tyr	Thr	Leu	Tyr	Glu	Phe	Phe	Ile	Val	Pro	Phe	Tyr	Lys	Ser	Val	Glu	755	760		765
Gly	Lys	Pro	Ser	Asn	Ser	Arg	Ile	Ala	Arg	Thr	Leu	Glu	Asp	Val	Pro	770	775		780
Ser	Glu	Ala	Pro	Tyr	Gly	Met	Glu	Ala	Leu	Leu	Leu	Asn	Ser	Ser	Ala	785	790		795
Val	Phe	Leu	Lys	Trp	Lys	Ala	Pro	Glu	Leu	Lys	Asp	Arg	His	Gly	Val	805	810		815

Leu	Leu	Asn	Tyr	His	Val	Ile	Val	Arg	Gly	Ile	Asp	Thr	Ala	His	Asn		
			820					825					830				
Phe	Ser	Arg	Ile	Leu	Thr	Asn	Val	Thr	Ile	Asp	Ala	Ala	Ser	Pro	Thr		
		835					840				845						
Leu	Val	Leu	Ala	Asn	Leu	Thr	Glu	Gly	Val	Met	Tyr	Thr	Val	Gly	Val		
	850					855				860							
Ala	Ala	Gly	Asn	Asn	Ala	Gly	Val	Gly	Pro	Tyr	Cys	Val	Pro	Ala	Thr		
865					870				875						880		
Leu	Arg	Leu	Asp	Pro	Ile	Thr	Lys	Arg	Leu	Asp	Pro	Phe	Ile	Asn	Gln		
			885					890						895			
Arg	Asp	His	Val	Asn	Asp	Val	Leu	Thr	Gln	Pro	Trp	Phe	Ile	Ile	Leu		
		900					905						910				
Leu	Gly	Ala	Ile	Leu	Ala	Val	Leu	Met	Leu	Ser	Phe	Gly	Ala	Met	Val		
	915					920						925					
Phe	Val	Lys	Arg	Lys	His	Met	Met	Met	Lys	Gln	Ser	Ala	Leu	Asn	Thr		
	930				935					940							
Met	Arg	Gly	Asn	His	Thr	Ser	Asp	Val	Leu	Lys	Met	Pro	Ser	Leu	Ser		
945					950				955						960		
Ala	Arg	Asn	Gly	Asn	Gly	Tyr	Trp	Leu	Asp	Ser	Ser	Thr	Gly	Gly	Met		
			965					970						975			
Val	Trp	Arg	Pro	Ser	Pro	Gly	Gly	Asp	Ser	Leu	Glu	Met	Gln	Lys	Asp		
		980				985							990				
His	Ile	Ala	Asp	Tyr	Ala	Pro	Val	Cys	Gly	Ala	Pro	Gly	Ser	Pro	Ala		
	995				1000							1005					
Gly	Gly	Gly	Thr	Ser	Ser	Gly	Gly	Ser	Gly	Gly	Ala	Gly	Ser	Gly	Ala		
	1010				1015							1020					
Ser	Gly	Gly	Asp	Asp	Ile	His	Gly	Gly	His	Gly	Ser	Glu	Arg	Asn	Gln		
1025					1030				1035					1040			
Gln	Arg	Tyr	Val	Gly	Glu	Tyr	Ser	Asn	Ile	Pro	Thr	Asp	Tyr	Ala	Glu		
			1045					1050						1055			
Val	Ser	Ser	Phe	Gly	Lys	Ala	Pro	Ser	Glu	Tyr	Gly	Arg	His	Gly	Asn		
		1060				1065							1070				
Ala	Ser	Pro	Ala	Pro	Tyr	Ala	Thr	Ser	Ser	Ile	Leu	Ser	Pro	His	Gln		
	1075					1080						1085					
Gln	Gln	Gln	Gln	Gln	Gln	Pro	Arg	Tyr	Gln	Gln	Arg	Pro	Val	Pro	Gly		
	1090				1095						1100						
Tyr	Gly	Leu	Gln	Arg	Pro	Met	His	Pro	His	Tyr	Gln	Gln	Gln	Gln	His		
1105					1110				1115						1120		
Gln	Gln	Gln	Gln	Ala	Gln	Gln	Thr	His	Gln	Gln	His	Gln	Ala	Leu	Gln		
			1125					1130						1135			
Gln	His	Gln	Gln	Leu	Pro	Pro	Ser	Asn	Ile	Tyr	Gln	Gln	Met	Ser	Thr		
		1140						1145					1150				
Thr	Ser	Glu	Ile	Tyr	Pro	Thr	Asn	Thr	Gly	Pro	Ser	Arg	Ser	Val	Tyr		
	1155					1160						1165					
Ser	Glu	Gln	Tyr	Tyr	Tyr	Pro	Lys	Asp	Lys	Gln	Arg	His	Ile	His	Ile		
	1170				1175				1180								
Thr	Glu	Asn	Lys	Leu	Ser	Asn	Cys	His	Thr	Tyr	Glu	Ala	Ala	Pro	Gly		
1185					1190				1195					1200			
Ala	Lys	Gln	Ser	Ser	Pro	Ile	Ser	Ser	Gln	Phe	Ala	Ser	Val	Arg	Arg		
			1205					1210						1215			
Gln	Gln	Leu	Pro	Pro	Asn	Cys	Ser	Ile	Gly	Arg	Glu	Ser	Ala	Arg	Phe		
		1220				1225							1230				
Lys	Val	Leu	Asn	Thr	Asp	Gln	Gly	Lys	Asn	Gln	Gln	Asn	Leu	Leu	Asp		
		1235				1240						1245					

Leu Asp Gly Ser Ser Met Cys Tyr Asn Gly Leu Ala Asp Ser Gly Cys
 1250 1255 1260
 Gly Gly Ser Pro Ser Pro Met Ala Met Leu Met Ser His Glu Asp Glu
 1265 1270 1275 1280
 His Ala Leu Tyr His Thr Ala Asp Gly Asp Leu Asp Asp Met Glu Arg
 1285 1290 1295
 Leu Tyr Val Lys Val Asp Glu Gln Gln Pro Pro Gln Gln Gln Gln Gln
 1300 1305 1310
 Leu Ile Pro Leu Val Pro Gln His Pro Ala Glu Gly His Leu Gln Ser
 1315 1320 1325
 Trp Arg Asn Gln Ser Thr Arg Ser Ser Arg Lys Asn Gly Gln Glu Cys
 1330 1335 1340
 Ile Lys Glu Pro Ser Glu Leu Ile Tyr Ala Pro Gly Ser Val Ala Ser
 1345 1350 1355 1360
 Glu Arg Ser Leu Leu Ser Asn Ser Gly Ser Gly Thr Ser Ser Gln Pro
 1365 1370 1375
 Ala Gly His Asn Val
 1380

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGTACTATC TAGGTTTTTA CCACACTCAC ACACACACAC ACACATACAT AAATTTTGAT	60
AAAATTCCTA ATGCCTCAAA TCTCGCTCCC GTGATAATCG AACATCCCAT CGATGTGGTG	120
GTATCTAGGG GATCGCCAGC AACCTCAAC TGTGGTGCAA AGCCATCTAC CGCCAAAATC	180
ACATGGTACA AGGATGGACA GCCCGTAATC ACGAATAAGG AGCAAGTGAA CAGCCACCGG	240
ATTGTTCTCG ACACGGGATC CCTGTTTCTT CTGAAAGTGA ATAGTGGAAA AAACGGAAAA	300
GACAGCGATG CGGGAGCGTA CTATTGTGTG GCCAGCAACG AGCACGGAGA AGTGAAGTCG	360
AACGAAGGAT CGTTAAAAAT GGCGATGCTT CGCGAAGACT TTCGAGTTCG GCCAAGAACA	420
GTTCAAGGTC TTGGTGAGGA GATGGCCGTT CTGGAATGCA GTCCGCCACG TGGATTCCCCG	480
GAGCCGGTTG TGAGCTGGCG GAAAGACGAC AAAGAGCTCC GAATTCAAGA CATGCCACGA	540
TACACTCTAC ACTCTGACGG AAACCTCATC ATTGATCCGG TCGATCGAAG CGATTCTGGT	600
ACTTATCAGT GTGTTGCCAA CAACATGGTC GGAGAACGGG TGTCCAATCC CGCAAGATTG	660
AGTGTCTTTG AGAAACCAAA GTTTGAGCAA GAACCCAAGG ACATGACGGT CGACGTCGGA	720
GCCGCAGTGC TGTTTGATTG TCGTGTGACT GGAGATCCTC AACCACAAAT TACGTGGAAA	780
CGCAAAAATG AGCCGATGCC AGTTACACGT GCATACATTG CCAAGGATAA TCGGGGGTTG	840
AGAATCGAAA GAGTTCAACC ATCAGACGAA GGTGAATACG TTTGCTATGC ACGAAATCCA	900
GCGGGAATC TTGAAGCATC TGCACATCTT CGTGTCCAGG CACCTCCATC CTTCCAGACA	960
AAACCAGCAG ACCAGTCAGT TCCAGCTGGA GGCACGGCAA CTTTGAATG CACCTTGGTC	1020
GGTCAACCGA GTCCCGCCTA TTTTGGAGC AAGGAAGGCC AACAGGATCT TCTTTTCCCA	1080
AGTTATGTGT CCGCTGATGG TAGAACGAAA GTTTCACCAA CTGGAACATT GACAATTGAG	1140
GAAGTTCGTC AAGTTGATGA GGGAGCTTAT GTGTGCGCTG GAATGAACTC GGCAGGAAGC	1200
TCGTTGAGCA AGGCAGCTTT GAAAGCAACA TTTGAAACCA AAGGCCGTGT CCAAAAAAAA	1260
AAGAGCAAAA TGGGCAAAAC GAAACAAAAA AATGTTCAAT CAATTATCAA ATATTTAATT	1320
TCAGCCGTGA CCGGAAACAC ACCCGCCAAA CCACCACCAA CAATCGAGCA TGGTCATCAA	1380
AATCAGACCC TTATGGTTGG ATCATCAGCC ATCCTTCCAT GTCAGGCTAG CGGAAAACCA	1440
ACTCCAGGAA TATCATGGCT CAGGGATGGG CTACCTATTG ACATTACAGA TAGTCGTATC	1500
AGTCAACATT CAACGGGAAG TCTACATATT GCCGATTAA AGAAACCTGA CACCGGAGTT	1560
TACACTTGCA TTGCGAAGAA CGAGGATGGA GAGTCAACAT GGTCGGCATC TCTGACTGTT	1620

GAAGATCACA	CTAGCAATGC	ACAATTTGTT	CGGATGCCGG	ATCCATCGAA	CTTCCCGTCT	1680
TCTCCAACGC	AACCCATTAT	TGTCAATGTC	ACTGATACCG	AAGTAGAGCT	CCACTGGAAT	1740
GCTCCCTCCA	CATCTGGCGC	AGGACCAATC	ACTGGTTATA	TCATTTCAGTA	CTACAGTCCA	1800
GACCTCGGAC	AGACGTGGTT	TAACATTCCA	GACTACGTGG	CATCTACTGA	ATATAGAATA	1860
AAGGGTCTGA	AACCATCTCA	CTCGTATATG	TTTGTGATTC	GAGCAGAAAA	TGAGAAAAGGT	1920
ATTGGAACGC	CGAGTGTGTC	GTCGGCTCTC	GTTACCACTA	GCAAGCCAGC	AGCTCAAGTT	1980
GCGCTTTCTG	ACAAGAACAA	AATGGACATG	GCCATCGCTG	AGAAGAGACT	CACTTCGGAA	2040
CAACTCATAA	AACTCGAGGA	AGTGAAGACT	ATTAATTCTA	CGGCCGTTCTG	TTTGTCTCTGG	2100
AAGAAGAGGA	AACTTGAAGA	GCTGATTGAT	GGTTACTACA	TCAAGTGGAG	AGGGCCTCCA	2160
AGAACCAATG	ATAATCAATA	CGTGAATGTG	ACCAGCCCTA	GCACCGAAAA	CTATGTTGTT	2220
TCAAATTTAA	TGCCATTAC	CAACTATGAG	TTTTTCGTGA	TTCTTATCA	TTCCGGAGTT	2280
CATAGTATTC	ATGGAGCACC	GAGTAATTCC	ATGGACGTGT	TGACCGCCGA	AGCTCCACCT	2340
TCATTGCCAC	CAGAGGATGT	GCGAATCCGT	ATGCTCAACC	TGACCACTCT	TCGTATCTCT	2400
TGGAAAGCAC	CAAAAGCCGA	CGGCATCAAC	GGAATTCTCA	AAGGATTCCA	AATTGTTATT	2460
GTTGGTCAAG	CGCCAACAA	CAATCGGAAC	ATCACTACAA	ACGAGAGAGC	TGCCAGTGTT	2520
ACTCTGTTCC	ATTTAGTGAC	TGGAATGACG	TATAAAATTC	GTGTAGCGGC	TAGAAGCAAT	2580
GGTGGAGTTG	GAGTCTCACA	TGGAACGAGT	GAAGTCATCA	TGAATCAAGA	CACGCTGGAA	2640
AAACACCTTG	CTGCTCAACA	AGAAAACGAA	TCATTTTTGT	ATGGGCTGAT	CAATAAATCT	2700
CATGTTCTCG	TGATTGTCAT	TGTTGCAATT	CTGATTATTT	TCGTAGTCAT	CATTATAGCC	2760
TATTGTTACT	GGAGGAATAG	CAGAAACAGT	GATGGAAAGG	ATCGAAGTTT	TATAAAGATC	2820
AATGATGGAA	GTGTTCATAT	GGCTTCGAAT	AATCTTTGGG	ATGTTGCACA	AAATCCGAAT	2880
CAGAAATCAA	TGTACAACAC	TGCTGGAAGA	ATGACTATGA	ACAATAGAAA	TGGCCAGGCT	2940
CTCTATTTCG	TGACACCAAA	TGCGCAAGAC	TTTTTCAACA	ATTGTGATGA	CTACAGTGGA	3000
ACGATGCACA	GACCAGGATC	CGAGCATCAC	TATCATTATG	CTCAACTGAC	TGGCGGACCT	3060
GGTAATGCGA	TGTCTACTTT	TTATGGAAAC	CAATATCACG	ATGATCCATC	TCCATATGCC	3120
ACCACAACAC	TGGTCTTGTC	GAACCAACAA	CCAGCTTGGC	TCAATGACAA	AATGCTTCGC	3180
GCGCCAGCAA	TGCCAACAAA	TCCCGTGCCA	CCAGAGCCAC	CGGCGCGATA	TGCAGATCAT	3240
ACCGCTGGAA	GACGATCTCG	ATCGAGCCGT	GCATCCGATG	GGAGAGGAAC	TCTGAATGGC	3300
GGACTCCATC	ACCGGACTAG	CGGAAGTCAA	CGGTCGGATA	GTCCACCTCA	CACAGATGTG	3360
AGCTATGTTT	AGCTTCACTC	ATCCGATGGA	ACTGGTAGTA	GTAAGGAAAG	AACTGGGGAG	3420
CGGAGAACAC	CACCGAATAA	GACTCTGATG	GACTTTATTC	CGCCACCACC	TTCCAATCCA	3480
CCACCACCTG	GAGGGCACGT	TTATGACACA	GCAACTAGGC	GTCAGTTGAA	TCGTGGAAAGT	3540
ACTCCACGAG	AAGACACCTA	CGATTGCGTC	AGTGACGGAG	CTTTTGCTCG	GGTTGATGTG	3600
AATGCAAGGC	CAACGAGTCG	GAATCGGAAT	TTGGGAGGAA	GGCCGCTGAA	AGGGAAACGA	3660
GACGACGATA	GTCAGCGGTC	TTCGTTGATG	ATGGACGATG	ATGGTGGATC	TTCTGAAGCT	3720
GACGGGGAGA	ACTCTGAAGG	AGACGTTCCG	CGTGGAGGTG	TTAGAAAAGC	AGTTCCTCGA	3780
ATGGGTATCT	CTGCAAGTAC	GCTGGCTCAT	AGTTGTTACG	GGACAAACGG	CACTGCTCAA	3840
CGATTCCGGT	CAATTCCACG	TAACAATGGA	ATCGTCACAC	AAGAACAAAC	TTGA	3894

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Tyr	Tyr	Leu	Gly	Phe	Tyr	His	Thr	His	Thr	His	Thr	His	Thr	Tyr
1				5					10					15	
Ile	Asn	Phe	Asp	Lys	Ile	Pro	Asn	Ala	Ser	Asn	Leu	Ala	Pro	Val	Ile
			20					25					30		
Ile	Glu	His	Pro	Ile	Asp	Val	Val	Val	Ser	Arg	Gly	Ser	Pro	Ala	Thr
		35					40					45			
Leu	Asn	Cys	Gly	Ala	Lys	Pro	Ser	Thr	Ala	Lys	Ile	Thr	Trp	Tyr	Lys

50	55	60													
Asp	Gly	Gln	Pro	Val	Ile	Thr	Asn	Lys	Glu	Gln	Val	Asn	Ser	His	Arg
65					70					75					80
Ile	Val	Leu	Asp	Thr	Gly	Ser	Leu	Phe	Leu	Leu	Lys	Val	Asn	Ser	Gly
				85					90						95
Lys	Asn	Gly	Lys	Asp	Ser	Asp	Ala	Gly	Ala	Tyr	Tyr	Cys	Val	Ala	Ser
			100					105					110		
Asn	Glu	His	Gly	Glu	Val	Lys	Ser	Asn	Glu	Gly	Ser	Leu	Lys	Leu	Ala
		115					120					125			
Met	Leu	Arg	Glu	Asp	Phe	Arg	Val	Arg	Pro	Arg	Thr	Val	Gln	Ala	Leu
	130					135					140				
Gly	Gly	Glu	Met	Ala	Val	Leu	Glu	Cys	Ser	Pro	Pro	Arg	Gly	Phe	Pro
145					150					155					160
Glu	Pro	Val	Val	Ser	Trp	Arg	Lys	Asp	Asp	Lys	Glu	Leu	Arg	Ile	Gln
			165					170						175	
Asp	Met	Pro	Arg	Tyr	Thr	Leu	His	Ser	Asp	Gly	Asn	Leu	Ile	Ile	Asp
		180						185				190			
Pro	Val	Asp	Arg	Ser	Asp	Ser	Gly	Thr	Tyr	Gln	Cys	Val	Ala	Asn	Asn
	195					200					205				
Met	Val	Gly	Glu	Arg	Val	Ser	Asn	Pro	Ala	Arg	Leu	Ser	Val	Phe	Glu
	210				215					220					
Lys	Pro	Lys	Phe	Glu	Gln	Glu	Pro	Lys	Asp	Met	Thr	Val	Asp	Val	Gly
225				230					235						240
Ala	Ala	Val	Leu	Phe	Asp	Cys	Arg	Val	Thr	Gly	Asp	Pro	Gln	Pro	Gln
			245					250					255		
Ile	Thr	Trp	Lys	Arg	Lys	Asn	Glu	Pro	Met	Pro	Val	Thr	Arg	Ala	Tyr
	260					265						270			
Ile	Ala	Lys	Asp	Asn	Arg	Gly	Leu	Arg	Ile	Glu	Arg	Val	Gln	Pro	Ser
	275			280								285			
Asp	Glu	Gly	Glu	Tyr	Val	Cys	Tyr	Ala	Arg	Asn	Pro	Ala	Gly	Thr	Leu
	290			295						300					
Glu	Ala	Ser	Ala	His	Leu	Arg	Val	Gln	Ala	Pro	Pro	Ser	Phe	Gln	Thr
305				310					315						320
Lys	Pro	Ala	Asp	Gln	Ser	Val	Pro	Ala	Gly	Gly	Thr	Ala	Thr	Phe	Glu
			325					330						335	
Cys	Thr	Leu	Val	Gly	Gln	Pro	Ser	Pro	Ala	Tyr	Phe	Trp	Ser	Lys	Glu
		340				345						350			
Gly	Gln	Gln	Asp	Leu	Leu	Phe	Pro	Ser	Tyr	Val	Ser	Ala	Asp	Gly	Arg
	355					360						365			
Thr	Lys	Val	Ser	Pro	Thr	Gly	Thr	Leu	Thr	Ile	Glu	Glu	Val	Arg	Gln
	370				375					380					
Val	Asp	Glu	Gly	Ala	Tyr	Val	Cys	Ala	Gly	Met	Asn	Ser	Ala	Gly	Ser
385				390					395						400
Ser	Leu	Ser	Lys	Ala	Ala	Leu	Lys	Ala	Thr	Phe	Glu	Thr	Lys	Gly	Arg
			405					410					415		
Val	Gln	Lys	Lys	Lys	Ser	Lys	Met	Gly	Lys	Gln	Lys	Gln	Lys	Asn	Val
		420					425					430			
Gln	Ser	Ile	Ile	Lys	Tyr	Leu	Ile	Ser	Ala	Val	Thr	Gly	Asn	Thr	Pro
	435					440					445				
Ala	Lys	Pro	Pro	Pro	Thr	Ile	Glu	His	Gly	His	Gln	Asn	Gln	Thr	Leu
	450				455				460						
Met	Val	Gly	Ser	Ser	Ala	Ile	Leu	Pro	Cys	Gln	Ala	Ser	Gly	Lys	Pro
465				470					475						480
Thr	Pro	Gly	Ile	Ser	Trp	Leu	Arg	Asp	Gly	Leu	Pro	Ile	Asp	Ile	Thr

485																490																495															
Asp	Ser	Arg	500			Ile	Ser	Gln	His	Ser	Thr	Gly	Ser	Leu	His	Ile	Ala	Asp																													
Leu	Lys	Lys	515			Pro	Asp	Thr	Gly	Val	Tyr	Thr	Cys	Ile	Ala	Lys	Asn	Glu																													
Asp	Gly	Glu	Ser	Thr	Trp	Ser	Ala	Ser	Leu	Thr	Val	Glu	Asp	His	Thr																																
Ser	Asn	Ala	Gln	Phe	Val	Arg	Met	Pro	Asp	Pro	Ser	Asn	Phe	Pro	Ser																																
545						550						555						560																													
Ser	Pro	Thr	Gln	Pro	Ile	Ile	Val	Asn	Val	Thr	Asp	Thr	Glu	Val	Glu																																
					565						570						575																														
Leu	His	Trp	Asn	Ala	Pro	Ser	Thr	Ser	Gly	Ala	Gly	Pro	Ile	Thr	Gly																																
					580						585						590																														
Tyr	Ile	Ile	Gln	Tyr	Tyr	Ser	Pro	Asp	Leu	Gly	Gln	Thr	Trp	Phe	Asn																																
					595						600						605																														
Ile	Pro	Asp	Tyr	Val	Ala	Ser	Thr	Glu	Tyr	Arg	Ile	Lys	Gly	Leu	Lys																																
					610						615						620																														
Pro	Ser	His	Ser	Tyr	Met	Phe	Val	Ile	Arg	Ala	Glu	Asn	Glu	Lys	Gly																																
625						630						635						640																													
Ile	Gly	Thr	Pro	Ser	Val	Ser	Ser	Ala	Leu	Val	Thr	Thr	Ser	Lys	Pro																																
					645						650						655																														
Ala	Ala	Gln	Val	Ala	Leu	Ser	Asp	Lys	Asn	Lys	Met	Asp	Met	Ala	Ile																																
					660						665						670																														
Ala	Glu	Lys	Arg	Leu	Thr	Ser	Glu	Gln	Leu	Ile	Lys	Leu	Glu	Glu	Val																																
					675						680						685																														
Lys	Thr	Ile	Asn	Ser	Thr	Ala	Val	Arg	Leu	Phe	Trp	Lys	Lys	Arg	Lys																																
					690						695						700																														
Leu	Glu	Glu	Leu	Ile	Asp	Gly	Tyr	Tyr	Ile	Lys	Trp	Arg	Gly	Pro	Pro																																
705						710						715						720																													
Arg	Thr	Asn	Asp	Asn	Gln	Tyr	Val	Asn	Val	Thr	Ser	Pro	Ser	Thr	Glu																																
					725						730						735																														
Asn	Tyr	Val	Val	Ser	Asn	Leu	Met	Pro	Phe	Thr	Asn	Tyr	Glu	Phe	Phe																																
					740						745						750																														
Val	Ile	Pro	Tyr	His	Ser	Gly	Val	His	Ser	Ile	His	Gly	Ala	Pro	Ser																																
					755						760						765																														
Asn	Ser	Met	Asp	Val	Leu	Thr	Ala	Glu	Ala	Pro	Pro	Ser	Leu	Pro	Pro																																
					770						775						780																														
Glu	Asp	Val	Arg	Ile	Arg	Met	Leu	Asn	Leu	Thr	Thr	Leu	Arg	Ile	Ser																																
785						790						795						800																													
Trp	Lys	Ala	Pro	Lys	Ala	Asp	Gly	Ile	Asn	Gly	Ile	Leu	Lys	Gly	Phe																																
					805						810						815																														
Gln	Ile	Val	Ile	Val	Gly	Gln	Ala	Pro	Asn	Asn	Asn	Arg	Asn	Ile	Thr																																
					820						825						830																														
Thr	Asn	Glu	Arg	Ala	Ala	Ser	Val	Thr	Leu	Phe	His	Leu	Val	Thr	Gly																																
					835						840						845																														
Met	Thr	Tyr	Lys	Ile	Arg	Val	Ala	Ala	Arg	Ser	Asn	Gly	Gly	Val	Gly																																
					850						855						860																														
Val	Ser	His	Gly	Thr	Ser	Glu	Val	Ile	Met	Asn	Gln	Asp	Thr	Leu	Glu																																
865						870						875						880																													
Lys	His	Leu	Ala	Ala	Gln	Gln	Glu	Asn	Glu	Ser	Phe	Leu	Tyr	Gly	Leu																																
					885</																																										

915	920	925
Asn Ser Asp Gly Lys Asp Arg Ser Phe Ile Lys Ile Asn Asp Gly Ser		
930	935	940
Val His Met Ala Ser Asn Asn Leu Trp Asp Val Ala Gln Asn Pro Asn		
945	950	955
Gln Asn Pro Met Tyr Asn Thr Ala Gly Arg Met Thr Met Asn Asn Arg		
	965	970
Asn Gly Gln Ala Leu Tyr Ser Leu Thr Pro Asn Ala Gln Asp Phe Phe		
	980	985
Asn Asn Cys Asp Asp Tyr Ser Gly Thr Met His Arg Pro Gly Ser Glu		
	995	1000
His His Tyr His Tyr Ala Gln Leu Thr Gly Gly Pro Gly Asn Ala Met		
	1010	1015
Ser Thr Phe Tyr Gly Asn Gln Tyr His Asp Asp Pro Ser Pro Tyr Ala		
1025	1030	1035
Thr Thr Thr Leu Val Leu Ser Asn Gln Gln Pro Ala Trp Leu Asn Asp		
	1045	1050
Lys Met Leu Arg Ala Pro Ala Met Pro Thr Asn Pro Val Pro Pro Glu		
	1060	1065
Pro Pro Ala Arg Tyr Ala Asp His Thr Ala Gly Arg Arg Ser Arg Ser		
	1075	1080
Ser Arg Ala Ser Asp Gly Arg Gly Thr Leu Asn Gly Gly Leu His His		
	1090	1095
Arg Thr Ser Gly Ser Gln Arg Ser Asp Ser Pro Pro His Thr Asp Val		
1105	1110	1115
Ser Tyr Val Gln Leu His Ser Ser Asp Gly Thr Gly Ser Ser Lys Glu		
	1125	1130
Arg Thr Gly Glu Arg Arg Thr Pro Pro Asn Lys Thr Leu Met Asp Phe		
	1140	1145
Ile Pro Pro Pro Pro Ser Asn Pro Pro Pro Gly Gly His Val Tyr		
	1155	1160
Asp Thr Ala Thr Arg Arg Gln Leu Asn Arg Gly Ser Thr Pro Arg Glu		
	1170	1175
Asp Thr Tyr Asp Ser Val Ser Asp Gly Ala Phe Ala Arg Val Asp Val		
1185	1190	1195
Asn Ala Arg Pro Thr Ser Arg Asn Arg Asn Leu Gly Gly Arg Pro Leu		
	1205	1210
Lys Gly Lys Arg Asp Asp Asp Ser Gln Arg Ser Ser Leu Met Met Asp		
	1220	1225
Asp Asp Gly Gly Ser Ser Glu Ala Asp Gly Glu Asn Ser Glu Gly Asp		
	1235	1240
Val Pro Arg Gly Gly Val Arg Lys Ala Val Pro Arg Met Gly Ile Ser		
	1250	1255
Ala Ser Thr Leu Ala His Ser Cys Tyr Gly Thr Asn Gly Thr Ala Gln		
1265	1270	1275
Arg Phe Arg Ser Ile Pro Arg Asn Asn Gly Ile Val Thr Gln Glu Gln		
	1285	1290
Thr		1295

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4956 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGAAATGGA	AACATGTTCC	TTTTTTGGTC	ATGATATCAC	TCCTCAGCTT	ATCCCCAAAT	60
CACCTGTTTC	TGGCCAGCT	TATTCCAGAC	CCTGAAGATG	TAGAGAGGGG	GAACGACCAC	120
GGGACGCCAA	TCCCCACCTC	TGATAACGAT	GACAATTTCG	TGGGCTATAC	AGGCTCCCGT	180
CTTCGTCAGG	AAGATTTTCC	ACCTCGCATT	GTTGAACACC	CTTCAGACCT	GATTGTCTCA	240
AAAGGAGAAC	CTGCAACTTT	GAAGTCAAAA	GCTGAAGGCC	GCCCCACACC	CACTATTGAA	300
TGGTACAAAG	GGGAGAGAG	AGTGGAGACA	GACAAAGATG	ACCCTCGCTC	ACACCGAATG	360
TTGCTGCCGA	GTGGATCTTT	ATTTTTCTTA	CGTATAGTAC	ATGGACGGAA	AAGTAGACCT	420
GATGAAGGAG	TCTATGTCTG	TGTAGCAAGG	AATTACCTTG	GAGAGGCTGT	GAGCCACAAT	480
GCATCGCTGG	AAGTAGCCAT	ACTTCGGGAT	GACTTCAGAC	AAAACCCCTC	GGATGTCATG	540
GTTGCAGTAG	GAGAGCCTGC	AGTAATGGAA	TGCCAACCTC	CACGAGGCCA	TCCTGAGCCC	600
ACCATTTTCAT	GGAAGAAAGA	TGGCTCTCCA	CTGGATGATA	AAGATGAAAG	AATAACTATA	660
CGAGGAGGAA	AGCTCATGAT	CACTTACACC	CGTAAAAGTG	ACGCTGGCAA	ATATGTTTGT	720
GTTGGTACCA	ATATGGTTGG	GGAACGTGAG	AGTGAAGTAG	CCGAGCTGAC	TGTCTTAGAG	780
AGACCATCAT	TTGTGAAGAG	ACCCAGTAAC	TTGGCAGTAA	CTGTGGATGA	CAGTGCAGAA	840
TTTAAATGTG	AGGCCCGAGG	TGACCCTGTA	CCTACAGTAC	GATGGAGGAA	AGATGATGGA	900
GAGCTGCCCA	AATCCAGATA	TGAAATCCGA	GATGATCATA	CCTTGAAAAT	TAGGAAGGTG	960
ACAGCTGGTG	ACATGGGTTT	ATACACTTGT	GTTGCAGAAA	ATATGGTGGG	CAAAGCTGAA	1020
GCATCTGCTA	CTCTGACTGT	TCAAGAACCT	CCACATTTTG	TTGTGAAACC	CCGTGACCAG	1080
GTTGTTGCTT	TGGGACGGAC	TGTAACCTTT	CAGTGTGAAG	CAACCGGAAA	TCCTCAACCA	1140
GCTATTTTCT	GGAGGAGAGA	AGGGAGTCAG	AATCTACTTT	TCTCATATCA	ACCACCACAG	1200
TCATCCAGCC	GATTTTCAGT	CTCCCAGACT	GGCGACCTCA	CAATTACTAA	TGTCCAGCGA	1260
TCTGATGTTG	GTTATTACAT	CTGCCAGACT	TTAAATGTTG	CTGGAAGCAT	CATCACAAAG	1320
GCATATTTGG	AAGTTACAGA	TGTGATTGCA	GATCGGCCTC	CCCCAGTTAT	TCGACAAGGT	1380
CCTGTGAATC	AGACTGTAGC	CGTGGATGGC	ACTTTCGTCC	TCAGCTGTGT	GGCCACAGGC	1440
AGTCCAGTGC	CCACCATCT	GTGGAGAAAG	GATGGAGTCC	TCGTTTCAAC	CCAAGACTCT	1500
CGAATCAAAC	AGTTGGAGAA	TGGAGTACTG	CAGATCCGAT	ATGCTAAGCT	GGGTGATACT	1560
GGTCGGTACA	CCTGCATTGC	ATCAACCCCC	AGTGGTGAAG	CAACATGGAG	TGCTTACATT	1620
GAAGTTCAAG	AATTTGGAGT	TCCAGTTCAG	CCTCCAAGAC	CTACTGACCC	AAATTTAATC	1680
CCTAGTGCCC	CATCAAAACC	TGAAGTGACA	GATGTCAGCA	GAAATACAGT	CACATTATCG	1740
TGGCAACCAA	ATTTGAATTC	AGGAGCAACT	CCAACATCTT	ATATTATAGA	AGCCTTCAGC	1800
CATGCATCTG	GTAGCAGCTG	GCAGACCGTA	GCAGAGAATG	TGAAAACAGA	AACATCTGCC	1860
ATTAAAGGAC	TCAAACCTAA	TGCAATTTAC	CTTTTCCTTG	TGAGGGCAGC	TAATGCATAT	1920
GGAATTAGTG	ATCCAAGCCA	AATATCAGAT	CCAGTGAAAA	CACAAGATGT	CCTACCAACA	1980
AGTCAGGGGG	TGGACCACAA	GCAGGTCCAG	AGAGAGCTGG	GAAATGCTGT	TCTGCACCTC	2040
CACAACCCCA	CCGTCTTTTC	TTCTCTTTCC	ATCGAAGTGC	ACTGGACAGT	AGATCAACAG	2100
TCTCAGTATA	TACAAGGATA	TAAAATTCTC	TATCGGCCAT	CTGGAGCCAA	CCACGGAGAA	2160
TCAGACTGGT	TAGTTTTTTGA	AGTGAGGACG	CCAGCCAAAA	ACAGTGTGGT	AATCCCTGAT	2220
CTCAGAAAGG	GAGTCAACTA	TGAAATTAAG	GCTCGCCCTT	TTTTTAATGA	ATTTCAAGGA	2280
GCAGATAGTG	AAATCAAGTT	TGCCAAAACC	CTGGAAGAAG	CACCCAGTGC	CCCACCCCAA	2340
GGTGTAAGTG	TATCCAAGAA	TGATGGAAAC	GGAAGTCAA	TTCTAGTTAG	TTGGCAGCCA	2400
CCTCCAGAAG	ACACTCAAAA	TGGAATGGTC	CAAGAGTATA	AGGTTTGGTG	TCTGGGCAAT	2460
GAAACTCGAT	ACCACATCAA	CAAAACAGTG	GATGGTTCCA	CCTTTTCCGT	GGTCATTCCC	2520
TTTCTTGTTT	CTGGAATCCG	ATACAGTGTG	GAAGTGGCAG	CCAGCACTGG	GGCTGGGTCT	2580
GGGGTAAAGA	GTGAGCCTCA	GTTTCATCCAG	CTGGATGCCC	ATGGAAACCC	TGTGTACACT	2640
GAGGACCAAG	TCAGCTTCGC	TCAGCAGATT	TCAGATGTGG	TGAAGCAGCC	GGCCTTCATA	2700
GCAGGTATTG	GAGCAGCCTG	TTGGATCATC	CTCATGGTCT	TCAGCATCTG	GCTTTATCGA	2760
CACCGCAAGA	AGAGAAAACG	ACTTACTAGT	ACCTACGCGG	GTATCAGAAA	AGTCCCGTCT	2820
TTTACCTTCA	CACCAACAGT	AACTTACCAG	AGAGGAGGCG	AAGCTGTCAG	CAGTGGAGGG	2880
AGGCCTGGAC	TTCTCAACAT	CAGTGAACCT	GCCGCGCAGC	CATGGCTGGC	AGACACGTGG	2940
CCTAATACTG	GCAACAACCA	CAATGACTGC	TCCATCAGCT	GCTGCACGGC	AGGCAATGGA	3000
AACAGCGACA	GCAACCTCAC	TACCTACAGT	CGCCAGCTG	ATTGTATAGC	AAATTATAAC	3060

AACCAACTGG	ATAACAAACA	AACAAATCTG	ATGCTCCCTG	AGTCAACTGT	TTATGGTGAT	3120
GTGGACCTTA	GTAACAAAAT	CAATGAGATG	AAAACCTTCA	ATAGCCCCAA	TCTGAAGGAT	3180
GGGCGTTTTG	TCAATCCATC	AGGGCAGCCT	ACTCCTTACG	CCACCACTCA	GCTCATCCAG	3240
TCAAACCTCA	GCAACAACAT	GAACAATGGC	AGCGGGGACT	CTGGCGAGAA	GCACTGGAAA	3300
CCACTGGGAC	AGCAGAAACA	AGAAGTGGCA	CCAGTTCAGT	ACAACATCGT	GGAGCAAAAC	3360
AAGCTGAACA	AAGATTATCG	AGCAAATGAC	ACAGTTCCTC	CAACTATCCC	ATACAACCAA	3420
TCATACGACC	AGAACACAGG	AGGATCCTAC	AACAGCTCAG	ACCGGGGCAG	TAGTACATCT	3480
GGGAGTCAGG	GGCACAAGAA	AGGGGCAAGA	ACACCCAAGG	TACCAAAACA	GGGTGGCATG	3540
AACTGGGCAG	ACCTGCTTCC	TCCTCCCCCA	GCACATCCTC	CTCCACACAG	CAATAGCGAA	3600
GAGTACAACA	TTTCTGTAGA	TGAAAGCTAT	GACCAAGAAA	TGCCATGTCC	CGTGCCACCA	3660
GCAAGGATGT	ATTTGCAACA	AGATGAATTA	GAAGAGGAGG	AAGATGAACG	AGGCCCCACT	3720
CCCCCTGTTT	GGGGAGCAGC	TTCTTCTCCA	GCTGCCGTGT	CCTATAGCCA	TCAGTCCACT	3780
GCCACTCTGA	CTCCCTCCCC	ACAGGAAGAA	CTCCAGCCCA	TGTTACAGGA	TTGTCCAGAG	3840
GAGACTGGCC	ACATGCAGCA	CCAGCCCCGAC	AGGAGACGGC	AGCCTGTGAG	TCCTCCTCCA	3900
CCACCACGGC	CGATCTCCCC	TCCACATACC	TATGGCTACA	TTTCAGGACC	CCTGGTCTCA	3960
GATATGGATA	CGGATGCGCC	AGAAGAGGAA	GAAGACGAAG	CCGACATGGA	GGTAGCCAAG	4020
ATGCAAACCA	GAAGGCTTTT	GTTACGTGGG	CTTGAGCAGA	CACCTGCCTC	CAGTGTTGGG	4080
GACCTGGAGA	GCTCTGTCAC	GGGGTCCATG	ATCAACGGCT	GGGGCTCAGC	CTCAGAGGAG	4140
GACAACATTT	CCAGCGGACG	CTCCAGTGTT	AGTTCCTCGG	ACGGCTCCTT	TTTCACTGAT	4200
GCTGACTTTG	CCCAGGCAGT	CGCAGCAGCG	GCAGAGTATG	CTGGTCTGAA	AGTAGCACGA	4260
CGGCAAATGC	AGGATGCTGC	TGGCCGTCGA	CATTTTTCATG	CGTCTCAGTG	CCCTAGGCCC	4320
ACAAGTCCCG	TGTCTACAGA	CAGCAACATG	AGTGCCGCCG	TAATGCAGAA	AACCAGACCA	4380
GCCAAGAAAC	TGAAACACCA	GCCAGGACAT	CTGCGCAGAG	AAACCTACAC	AGATGATCTT	4440
CCACCACCTC	CTGTGCCGCC	ACCTGCTATA	AAGTCACCTA	CTGCCCAATC	CAAGACACAG	4500
CTGGAAGTAC	GACCTGTAGT	GGTGCCAAAA	CTCCCTTCTA	TGGATGCAAG	AACAGACAGA	4560
TCATCAGACA	GAAAAGGAAG	CAGTTACAAG	GGGAGAGAAG	TGTTGGATGG	AAGACAGGTT	4620
GTTGACATGC	GAACAAATCC	AGGTGATCCC	AGAGAAGCAC	AGGAACAGCA	AAATGACGGG	4680
AAAGGACGTG	GAAACAAGGC	AGCAAAACGA	GACCTTCCAC	CAGCAAAGAC	TCATCTCATC	4740
CAAGAGGATA	TTCTACCTTA	TTGTAGACCT	ACTTTTCCAA	CATCAAATAA	TCCCAGAGAT	4800
CCCAGTTCCT	CAAGCTCAAT	GTCATCAAGA	GGATCAGGAA	GCAGACAAAG	AGAACAAGCA	4860
AATGTAGGTC	GAAGAAATAT	TGCAGAAATG	CAGGTACTTG	GAGGATATGA	AAGAGGAGAA	4920
GATAATAATG	AAGAATTAGA	GGAAACTGAA	AGCTGA			4956

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1651 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Lys	Trp	Lys	His	Val	Pro	Phe	Leu	Val	Met	Ile	Ser	Leu	Leu	Ser
1				5				10					15		
Leu	Ser	Pro	Asn	His	Leu	Phe	Leu	Ala	Gln	Leu	Ile	Pro	Asp	Pro	Glu
			20					25					30		
Asp	Val	Glu	Arg	Gly	Asn	Asp	His	Gly	Thr	Pro	Ile	Pro	Thr	Ser	Asp
			35				40						45		
Asn	Asp	Asp	Asn	Ser	Leu	Gly	Tyr	Thr	Gly	Ser	Arg	Leu	Arg	Gln	Glu
			50				55				60				
Asp	Phe	Pro	Pro	Arg	Ile	Val	Glu	His	Pro	Ser	Asp	Leu	Ile	Val	Ser
			65			70				75				80	
Lys	Gly	Glu	Pro	Ala	Thr	Leu	Asn	Cys	Lys	Ala	Glu	Gly	Arg	Pro	Thr
			85					90					95		
Pro	Thr	Ile	Glu	Trp	Tyr	Lys	Gly	Gly	Glu	Arg	Val	Glu	Thr	Asp	Lys

[illegible]

530		535		540
Phe Gly Val Pro Val Gln Pro Pro Arg Pro Thr Asp Pro Asn Leu Ile				
545		550		560
Pro Ser Ala Pro Ser Lys Pro Glu Val Thr Asp Val Ser Arg Asn Thr				
	565		570	575
Val Thr Leu Ser Trp Gln Pro Asn Leu Asn Ser Gly Ala Thr Pro Thr				
	580		585	590
Ser Tyr Ile Ile Glu Ala Phe Ser His Ala Ser Gly Ser Ser Trp Gln				
	595		600	605
Thr Val Ala Glu Asn Val Lys Thr Glu Thr Ser Ala Ile Lys Gly Leu				
	610		615	620
Lys Pro Asn Ala Ile Tyr Leu Phe Leu Val Arg Ala Ala Asn Ala Tyr				
625		630		640
Gly Ile Ser Asp Pro Ser Gln Ile Ser Asp Pro Val Lys Thr Gln Asp				
	645		650	655
Val Leu Pro Thr Ser Gln Gly Val Asp His Lys Gln Val Gln Arg Glu				
	660		665	670
Leu Gly Asn Ala Val Leu His Leu His Asn Pro Thr Val Leu Ser Ser				
	675		680	685
Ser Ser Ile Glu Val His Trp Thr Val Asp Gln Gln Ser Gln Tyr Ile				
	690		695	700
Gln Gly Tyr Lys Ile Leu Tyr Arg Pro Ser Gly Ala Asn His Gly Glu				
705		710		720
Ser Asp Trp Leu Val Phe Glu Val Arg Thr Pro Ala Lys Asn Ser Val				
	725		730	735
Val Ile Pro Asp Leu Arg Lys Gly Val Asn Tyr Glu Ile Lys Ala Arg				
	740		745	750
Pro Phe Phe Asn Glu Phe Gln Gly Ala Asp Ser Glu Ile Lys Phe Ala				
	755		760	765
Lys Thr Leu Glu Glu Ala Pro Ser Ala Pro Pro Gln Gly Val Thr Val				
	770		775	780
Ser Lys Asn Asp Gly Asn Gly Thr Ala Ile Leu Val Ser Trp Gln Pro				
785		790		800
Pro Pro Glu Asp Thr Gln Asn Gly Met Val Gln Glu Tyr Lys Val Trp				
	805		810	815
Cys Leu Gly Asn Glu Thr Arg Tyr His Ile Asn Lys Thr Val Asp Gly				
	820		825	830
Ser Thr Phe Ser Val Val Ile Pro Phe Leu Val Pro Gly Ile Arg Tyr				
	835		840	845
Ser Val Glu Val Ala Ala Ser Thr Gly Ala Gly Ser Gly Val Lys Ser				
	850		855	860
Glu Pro Gln Phe Ile Gln Leu Asp Ala His Gly Asn Pro Val Ser Pro				
865		870		880
Glu Asp Gln Val Ser Leu Ala Gln Gln Ile Ser Asp Val Val Lys Gln				
	885		890	895
Pro Ala Phe Ile Ala Gly Ile Gly Ala Ala Cys Trp Ile Ile Leu Met				
	900		905	910
Val Phe Ser Ile Trp Leu Tyr Arg His Arg Lys Lys Arg Asn Gly Leu				
	915		920	925
Thr Ser Thr Tyr Ala Gly Ile Arg Lys Val Pro Ser Phe Thr Phe Thr				
	930		935	940
Pro Thr Val Thr Tyr Gln Arg Gly Gly Glu Ala Val Ser Ser Gly Gly				
945		950		960
Arg Pro Gly Leu Leu Asn Ile Ser Glu Pro Ala Ala Gln Pro Trp Leu				

														965															970															975											
Ala	Asp	Thr	Trp				Pro	Asn	Thr	Gly	Asn	Asn	His	Asn	Asp	Cys	Ser	Ile																																					
														980															985															990											
Ser	Cys	Cys	Thr	Ala	Gly	Asn	Gly	Asn	Ser	Asp	Ser	Asn	Leu	Thr	Thr																																								
														995															1000															1005											
Tyr	Ser	Arg	Pro	Ala	Asp	Cys	Ile	Ala	Asn	Tyr	Asn	Asn	Gln	Leu	Asp																																								
														1010															1015															1020											
Asn	Lys	Gln	Thr	Asn	Leu	Met	Leu	Pro	Glu	Ser	Thr	Val	Tyr	Gly	Asp																																								
1025														1030														1035														1040													
Val	Asp	Leu	Ser	Asn	Lys	Ile	Asn	Glu	Met	Lys	Thr	Phe	Asn	Ser	Pro																																								
														1045														1050														1055													
Asn	Leu	Lys	Asp	Gly	Arg	Phe	Val	Asn	Pro	Ser	Gly	Gln	Pro	Thr	Pro																																								
														1060														1065														1070													
Tyr	Ala	Thr	Thr	Gln	Leu	Ile	Gln	Ser	Asn	Leu	Ser	Asn	Asn	Met	Asn																																								
														1075														1080														1085													
Asn	Gly	Ser	Gly	Asp	Ser	Gly	Glu	Lys	His	Trp	Lys	Pro	Leu	Gly	Gln																																								
1090														1095														1100																											
Gln	Lys	Gln	Glu	Val	Ala	Pro	Val	Gln	Tyr	Asn	Ile	Val	Glu	Gln	Asn																																								
1105														1110														1115														1120													
Lys	Leu	Asn	Lys	Asp	Tyr	Arg	Ala	Asn	Asp	Thr	Val	Pro	Pro	Thr	Ile																																								
														1125														1130														1135													
Pro	Tyr	Asn	Gln	Ser	Tyr	Asp	Gln	Asn	Thr	Gly	Gly	Ser	Tyr	Asn	Ser																																								
														1140														1145														1150													
Ser	Asp	Arg	Gly	Ser	Ser	Thr	Ser	Gly	Ser	Gln	Gly	His	Lys	Lys	Gly																																								
1155														1160														1165																											
Ala	Arg	Thr	Pro	Lys	Val	Pro	Lys	Gln	Gly	Gly	Met	Asn	Trp	Ala	Asp																																								
1170														1175														1180																											
Leu	Leu	Pro	Pro	Pro	Pro	Ala	His	Pro	Pro	Pro	His	Ser	Asn	Ser	Glu																																								
1185														1190														1195														1200													
Glu	Tyr	Asn	Ile	Ser	Val	Asp	Glu	Ser	Tyr	Asp	Gln	Glu	Met	Pro	Cys																																								
														1205														1210														1215													
Pro	Val	Pro	Pro	Ala	Arg	Met	Tyr	Leu	Gln	Gln	Asp	Glu	Leu	Glu	Glu																																								
														1220														1225														1230													
Glu	Glu	Asp	Glu	Arg	Gly	Pro	Thr	Pro	Pro	Val	Arg	Gly	Ala	Ala	Ser																																								
1235														1240														1245																											
Ser	Pro	Ala	Ala	Val	Ser	Tyr	Ser	His	Gln	Ser	Thr	Ala	Thr	Leu	Thr																																								
1250														1255														1260																											
Pro	Ser	Pro	Gln	Glu	Glu	Leu	Gln	Pro	Met	Leu	Gln	Asp	Cys	Pro	Glu																																								
1265														1270														1275														1280													
Glu	Thr	Gly	His	Met	Gln	His	Gln	Pro	Asp	Arg	Arg	Arg	Gln	Pro	Val																																								
														1285														1290														1295													
Ser	Pro	Pro	Pro	Pro	Pro	Arg	Pro	Ile	Ser	Pro	Pro	His	Thr	Tyr	Gly																																								
														1300														1305														1310													
Tyr	Ile	Ser	Gly	Pro	Leu	Val	Ser	Asp	Met	Asp	Thr	Asp	Ala	Pro	Glu																																								
1315														1320														1325																											
Glu	Glu	Glu	Asp	Glu	Ala	Asp	Met	Glu	Val	Ala	Lys	Met	Gln	Thr	Arg																																								
1330														1335														1340																											
Arg	Leu	Leu	Leu	Arg	Gly	Leu	Glu	Gln	Thr	Pro	Ala	Ser	Ser	Val	Gly																																								
1345														1350														1355														1360													
Asp	Leu	Glu	Ser	Ser	Val	Thr	Gly	Ser	Met	Ile	Asn	Gly																																											

1395	1400	1405
Ala Ala Ala Glu Tyr Ala Gly Leu Lys Val Ala Arg Arg Gln Met Gln		
1410	1415	1420
Asp Ala Ala Gly Arg Arg His Phe His Ala Ser Gln Cys Pro Arg Pro		
1425	1430	1435
Thr Ser Pro Val Ser Thr Asp Ser Asn Met Ser Ala Ala Val Met Gln		
	1445	1450
Lys Thr Arg Pro Ala Lys Lys Leu Lys His Gln Pro Gly His Leu Arg		
	1460	1465
Arg Glu Thr Tyr Thr Asp Asp Leu Pro Pro Pro Pro Val Pro Pro Pro		
	1475	1480
Ala Ile Lys Ser Pro Thr Ala Gln Ser Lys Thr Gln Leu Glu Val Arg		
	1490	1495
Pro Val Val Val Pro Lys Leu Pro Ser Met Asp Ala Arg Thr Asp Arg		
1505	1510	1515
Ser Ser Asp Arg Lys Gly Ser Ser Tyr Lys Gly Arg Glu Val Leu Asp		
	1525	1530
Gly Arg Gln Val Val Asp Met Arg Thr Asn Pro Gly Asp Pro Arg Glu		
	1540	1545
Ala Gln Glu Gln Gln Asn Asp Gly Lys Gly Arg Gly Asn Lys Ala Ala		
	1555	1560
Lys Arg Asp Leu Pro Pro Ala Lys Thr His Leu Ile Gln Glu Asp Ile		
	1570	1575
Leu Pro Tyr Cys Arg Pro Thr Phe Pro Thr Ser Asn Asn Pro Arg Asp		
1585	1590	1595
Pro Ser Ser Ser Ser Ser Met Ser Ser Arg Gly Ser Gly Ser Arg Gln		
	1605	1610
Arg Glu Gln Ala Asn Val Gly Arg Arg Asn Ile Ala Glu Met Gln Val		
	1620	1625
Leu Gly Gly Tyr Glu Arg Gly Glu Asp Asn Asn Glu Glu Leu Glu Glu		
	1635	1640
Thr Glu Ser		1645
1650		

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 855..1187
- (D) OTHER INFORMATION: /note= "N signifies gap in sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CAGATTGTTG CTCAAGGTCG AACAGTGACA TTTCCCTGTG AAATAAAGG AAACCCACAG	60
CCAGCTGTTT TTTGGCAGAA AGAAGGCAGC CAGAACCTAC TTTTCCCAAA CCAACCCAG	120
CAGCCCAACA GTAGATGCTC AGTGTCACCA ACTGGAGACC TCACAATCAC CAACATTCAA	180
CGTTCGACG CGGGTTACTA CATCTGCCAG GCTTTAACTG TGGCAGGAAG CATTTTAGCA	240
AAAGCTCAAC TGGAGGTTAC TGATGTTTTG ACAGATAGAC CTCCACCTAT AATTCTACAA	300
GGCCAGCCA ACCAAACGCT GGCAGTGGAT GGTACAGCGT TACTGAAATG TAAAGCCACT	360
GGTGATCCTC TTCCTGTAAT TAGCTGGTTA AAGGAGGGAT TTACTTTTCC GGGTAGAGAT	420
CCAAGAGCAA CAATTCAAGA GCAAGGCACA CTGCAGATTA AGAATTTACG GATTCTGTAT	480

ACTGGCACTT	ATACTTGTGT	GGCTACAAGT	TCAAGTGGAG	AGGCTTCCTG	GAGTGCAGTG	540
CTGGATGTGA	CAGAGTCTGG	AGCAACAATC	AGTAAAAACT	ATGATTTAAG	TGACCTGCCA	600
GGGCCACCAT	CCAAACCGCA	AGTCACTGAT	GTTACTAAGA	ACAGTGTAC	CTTGTCCTGG	660
CAGCCAGGTA	CCCCTGGAAC	CCTTCCAGCA	AGTGCATATA	TCATTGAGGC	TTTCAGCCAA	720
TCAGTGAGCA	ACAGCTGGCA	GACCGTGGCA	AACCATGTAA	AGACCACCCT	CTATACTGTA	780
AGAGGACTGC	GGCCCAATAC	AATCTACTTA	TTCATGGTCA	GAGCGATCAA	CCCCAAGGTY	840
TCAGTGACCC	AAGTNAAACC	ACAGAAAAAC	AATGGATCCA	CTTGGGCCAA	TGTCCCTCTA	900
CCTCCCCCCC	CAGTCCAGCC	CCTTCCTGGC	ACGGAGCTGG	AACACTATGC	AGTGGAACAA	960
CAAGAAAATG	GCTATGACAG	TGATAGCTGG	TGCCCACCAT	TGCCAGTACA	AACTTACTTA	1020
CACCAAGGTC	TGGAAGATGA	ACTGGAAGAA	GATGATGATA	GGGTCCCAAC	ACCTCCTGTT	1080
CGAGGCGTGG	CTTCTTCTCC	TGCTATCTCC	TTTGGACAGC	AGTCCACTGC	AACTCTTACT	1140
CCATCCCCAC	GGGAAGAGAT	GCAACCCATG	CTGCAGGCTT	CACCTNTTTA	CCTCCTCTCA	1200
AAGACCTCGA	CCTACCAGCC	CATTTTCTAC	TGACAGTAAC	ACCAGTGCAG	CCCTGAGTCA	1260
AAGTCAGAGG	CCTCGGCCCA	CTAAAAAACA	CAAGGGAGGG			1300

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 285..396
- (D) OTHER INFORMATION: /note= "Xaa signifies gap in sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gln	Ile	Val	Ala	Gln	Gly	Arg	Thr	Val	Thr	Phe	Pro	Cys	Glu	Thr	Lys
1				5					10					15	
Gly	Asn	Pro	Gln	Pro	Ala	Val	Phe	Trp	Gln	Lys	Glu	Gly	Ser	Gln	Asn
			20					25					30		
Leu	Leu	Phe	Pro	Asn	Gln	Pro	Gln	Gln	Pro	Asn	Ser	Arg	Cys	Ser	Val
		35					40					45			
Ser	Pro	Thr	Gly	Asp	Leu	Thr	Ile	Thr	Asn	Ile	Gln	Arg	Ser	Asp	Ala
	50					55				60					
Gly	Tyr	Tyr	Ile	Cys	Gln	Ala	Leu	Thr	Val	Ala	Gly	Ser	Ile	Leu	Ala
65					70				75					80	
Lys	Ala	Gln	Leu	Glu	Val	Thr	Asp	Val	Leu	Thr	Asp	Arg	Pro	Pro	Pro
			85					90					95		
Ile	Ile	Leu	Gln	Gly	Pro	Ala	Asn	Gln	Thr	Leu	Ala	Val	Asp	Gly	Thr
		100					105					110			
Ala	Leu	Leu	Lys	Cys	Lys	Ala	Thr	Gly	Asp	Pro	Leu	Pro	Val	Ile	Ser
	115						120					125			
Trp	Leu	Lys	Glu	Gly	Phe	Thr	Phe	Pro	Gly	Arg	Asp	Pro	Arg	Ala	Thr
	130					135				140					
Ile	Gln	Glu	Gln	Gly	Thr	Leu	Gln	Ile	Lys	Asn	Leu	Arg	Ile	Ser	Asp
145					150				155					160	
Thr	Gly	Thr	Tyr	Thr	Cys	Val	Ala	Thr	Ser	Ser	Ser	Gly	Glu	Ala	Ser
			165					170					175		
Trp	Ser	Ala	Val	Leu	Asp	Val	Thr	Glu	Ser	Gly	Ala	Thr	Ile	Ser	Lys
		180					185					190			
Asn	Tyr	Asp	Leu	Ser	Asp	Leu	Pro	Gly	Pro	Pro	Ser	Lys	Pro	Gln	Val
	195					200					205				
Thr	Asp	Val	Thr	Lys	Asn	Ser	Val	Thr	Leu	Ser	Trp	Gln	Pro	Gly	Thr

210	215	220
Pro Gly Thr Leu Pro Ala Ser Ala Tyr Ile Ile Glu Ala Phe Ser Gln		
225	230	235
Ser Val Ser Asn Ser Trp Gln Thr Val Ala Asn His Val Lys Thr Thr		240
	245	250
Leu Tyr Thr Val Arg Gly Leu Arg Pro Asn Thr Ile Tyr Leu Phe Met		255
	260	265
Val Arg Ala Ile Asn Pro Lys Val Ser Val Thr Gln Xaa Lys Pro Gln		270
	275	280
Lys Asn Asn Gly Ser Thr Trp Ala Asn Val Pro Leu Pro Pro Pro Pro		285
	290	295
Val Gln Pro Leu Pro Gly Thr Glu Leu Glu His Tyr Ala Val Glu Gln		300
305	310	315
Gln Glu Asn Gly Tyr Asp Ser Asp Ser Trp Cys Pro Pro Leu Pro Val		320
	325	330
Gln Thr Tyr Leu His Gln Gly Leu Glu Asp Glu Leu Glu Glu Asp Asp		335
	340	345
Asp Arg Val Pro Thr Pro Pro Val Arg Gly Val Ala Ser Ser Pro Ala		350
	355	360
Ile Ser Phe Gly Gln Gln Ser Thr Ala Thr Leu Thr Pro Ser Pro Arg		365
370	375	380
Glu Glu Met Gln Pro Met Leu Gln Ala Ser Pro Xaa Phe Thr Ser Ser		
385	390	395
Gln Arg Pro Arg Pro Thr Ser Pro Phe Ser Thr Asp Ser Asn Thr Ser		400
	405	410
Ala Ala Leu Ser Gln Ser Gln Arg Pro Arg Pro Thr Lys Lys His Lys		415
	420	425
Gly Gly		430

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCCCAGGCAG TTGCTGCAGC TGC GGAGTAT GCGGGCCTGA AAGTGGCTCG CCGCCAAATG	60
CAAGATGCTG CTGGCCGCCG CCACTTCCAT GCCTCTCAGT GCCCAAGGCC CACGAGTCCT	120
GTGTCCACAG ACAGCAACAT GAGTGCTGTT GTGATCCAGA AAGCCAGACC CGCCAAGAAG	180
CAGAAACACC AGCCAGGACA TCTGCGCAGG GAAGCCTACG CAGATGATCT TCCACCCCT	240
CCAGTGCCAC CACCTGCTAT AAAATCGCCC ACTGTCCAGT CCAAGGCACA GCTGGAGGTA	300
CGGCCTGTCA TGGTGCCAAA ACTCGCGTCT ATAGAAGCAA GGACAGATAG ATCGTCAGAC	360
AGAAAAGGAG GCAGTTACAA GGGGAGAGAA GCTCTGGATG GAAGACAAGT CACTGACCTG	420
CGAACAAATC CAAGTGACCC CAGA	444

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ala	Gln	Ala	Val	Ala	Ala	Ala	Ala	Glu	Tyr	Ala	Gly	Leu	Lys	Val	Ala
1				5					10					15	
Arg	Arg	Gln	Met	Gln	Asp	Ala	Ala	Gly	Arg	Arg	His	Phe	His	Ala	Ser
		20						25						30	
Gln	Cys	Pro	Arg	Pro	Thr	Ser	Pro	Val	Ser	Thr	Asp	Ser	Asn	Met	Ser
		35					40					45			
Ala	Val	Val	Ile	Gln	Lys	Ala	Arg	Pro	Ala	Lys	Lys	Gln	Lys	His	Gln
	50					55					60				
Pro	Gly	His	Leu	Arg	Arg	Glu	Ala	Tyr	Ala	Asp	Asp	Leu	Pro	Pro	Pro
65					70					75				80	
Pro	Val	Pro	Pro	Pro	Ala	Ile	Lys	Ser	Pro	Thr	Val	Gln	Ser	Lys	Ala
				85				90						95	
Gln	Leu	Glu	Val	Arg	Pro	Val	Met	Val	Pro	Lys	Leu	Ala	Ser	Ile	Glu
			100					105					110		
Ala	Arg	Thr	Asp	Arg	Ser	Ser	Asp	Arg	Lys	Gly	Gly	Ser	Tyr	Lys	Gly
		115					120					125			
Arg	Glu	Ala	Leu	Asp	Gly	Arg	Gln	Val	Thr	Asp	Leu	Arg	Thr	Asn	Pro
	130					135					140				
Ser	Asp	Pro	Arg												
145															

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 909 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Phe	Asn	Arg	Lys	Thr	Leu	Leu	Cys	Thr	Ile	Leu	Leu	Val	Leu	Gln
1				5					10					15	
Ala	Val	Ile	Arg	Ser	Phe	Cys	Glu	Asp	Ala	Ser	Asn	Leu	Ala	Pro	Val
		20						25					30		
Ile	Ile	Glu	His	Pro	Ile	Asp	Val	Val	Val	Ser	Arg	Gly	Ser	Pro	Ala
		35				40						45			
Thr	Leu	Asn	Cys	Gly	Ala	Lys	Pro	Ser	Thr	Ala	Lys	Ile	Thr	Trp	Tyr
	50					55				60					
Lys	Asp	Gly	Gln	Pro	Val	Ile	Thr	Asn	Lys	Glu	Gln	Val	Asn	Ser	His
65				70					75					80	
Arg	Ile	Val	Leu	Asp	Thr	Gly	Ser	Leu	Phe	Leu	Leu	Lys	Val	Asn	Ser
			85					90					95		
Gly	Lys	Asn	Gly	Lys	Asp	Ser	Asp	Ala	Gly	Ala	Tyr	Tyr	Cys	Val	Ala
		100					105					110			
Ser	Asn	Glu	His	Gly	Glu	Val	Lys	Ser	Asn	Glu	Gly	Ser	Leu	Lys	Leu
	115					120					125				
Ala	Met	Leu	Arg	Glu	Asp	Phe	Arg	Val	Arg	Pro	Arg	Thr	Val	Gln	Ala
	130					135				140					
Leu	Gly	Gly	Glu	Met	Ala	Val	Leu	Glu	Cys	Ser	Pro	Pro	Arg	Gly	Phe
145				150					155				160		
Pro	Glu	Pro	Val	Val	Ser	Trp	Arg	Lys	Asp	Asp	Lys	Glu	Leu	Arg	Ile
			165					170				175			
Gln	Asp	Met	Pro	Arg	Tyr	Thr	Leu	His	Ser	Asp	Gly	Asn	Leu	Ile	Ile
			180				185					190			

Asp	Pro	Val	Asp	Arg	Ser	Asp	Ser	Gly	Thr	Tyr	Gln	Cys	Val	Ala	Asn		
		195					200					205					
Asn	Met	Val	Gly	Glu	Arg	Val	Ser	Asn	Pro	Ala	Arg	Leu	Ser	Val	Phe		
		210					215				220						
Glu	Lys	Pro	Lys	Phe	Glu	Gln	Glu	Pro	Lys	Asp	Met	Thr	Val	Asp	Val		
225					230					235					240		
Gly	Ala	Ala	Val	Leu	Phe	Asp	Cys	Arg	Val	Thr	Gly	Asp	Pro	Gln	Pro		
				245					250					255			
Gln	Ile	Thr	Trp	Lys	Arg	Lys	Asn	Glu	Pro	Met	Pro	Val	Thr	Arg	Ala		
			260					265					270				
Tyr	Ile	Ala	Lys	Asp	Asn	Arg	Gly	Leu	Arg	Ile	Glu	Arg	Val	Gln	Pro		
		275					280					285					
Ser	Asp	Glu	Gly	Glu	Tyr	Val	Cys	Tyr	Ala	Arg	Asn	Pro	Ala	Gly	Thr		
		290				295					300						
Leu	Glu	Ala	Ser	Ala	His	Leu	Arg	Val	Gln	Ala	Pro	Pro	Ser	Phe	Gln		
305					310				315						320		
Thr	Lys	Pro	Ala	Asp	Gln	Ser	Val	Pro	Ala	Gly	Gly	Thr	Ala	Thr	Phe		
				325					330					335			
Glu	Cys	Thr	Leu	Val	Gly	Gln	Pro	Ser	Pro	Ala	Tyr	Phe	Trp	Ser	Lys		
			340					345					350				
Glu	Gly	Gln	Gln	Asp	Leu	Leu	Phe	Pro	Ser	Tyr	Val	Ser	Ala	Asp	Gly		
		355				360					365						
Arg	Thr	Lys	Val	Ser	Pro	Thr	Gly	Thr	Leu	Thr	Ile	Glu	Glu	Val	Arg		
						375					380						
Gln	Val	Asp	Glu	Gly	Ala	Tyr	Val	Cys	Ala	Gly	Met	Asn	Ser	Ala	Gly		
385					390					395					400		
Ser	Ser	Leu	Ser	Lys	Ala	Ala	Leu	Lys	Val	Thr	Thr	Lys	Ala	Val	Thr		
				405					410					415			
Gly	Asn	Thr	Pro	Ala	Lys	Pro	Pro	Pro	Thr	Ile	Glu	His	Gly	His	Gln		
			420					425					430				
Asn	Gln	Thr	Leu	Met	Val	Gly	Ser	Ser	Ala	Ile	Leu	Pro	Cys	Gln	Ala		
		435					440					445					
Ser	Gly	Lys	Pro	Thr	Pro	Gly	Ile	Ser	Trp	Leu	Arg	Asp	Gly	Leu	Pro		
		450				455					460						
Ile	Asp	Ile	Thr	Asp	Ser	Arg	Ile	Ser	Gln	His	Ser	Thr	Gly	Ser	Leu		
465					470				475						480		
His	Ile	Ala	Asp	Leu	Lys	Lys	Pro	Asp	Thr	Gly	Val	Tyr	Thr	Cys	Ile		
				485					490					495			
Ala	Lys	Asn	Glu	Asp	Gly	Glu	Ser	Thr	Trp	Ser	Ala	Ser	Leu	Thr	Val		
			500					505					510				
Glu	Asp	His	Thr	Ser	Asn	Ala	Gln	Phe	Val	Arg	Met	Pro	Asp	Pro	Ser		
		515					520					525					
Asn	Phe	Pro	Ser	Ser	Pro	Thr	Gln	Pro	Ile	Ile	Val	Asn	Val	Thr	Asp		
		530				535					540						
Thr	Glu	Val	Glu	Leu	His	Trp	Asn	Ala	Pro	Ser	Thr	Ser	Gly	Ala	Gly		
545					550					555					560		
Pro	Ile	Thr	Gly	Tyr	Ile	Ile	Gln	Tyr	Tyr	Ser	Pro	Asp	Leu	Gly	Gln		
				565				570						575			
Thr	Trp	Phe	Asn	Ile	Pro	Asp	Tyr	Val	Ala	Ser	Thr	Glu	Tyr	Arg	Ile		
			580					585					590				
Lys	Gly	Leu	Lys	Pro	Ser	His	Ser	Tyr	Met	Phe	Val	Ile	Arg	Ala	Glu		
		595				600					605						
Asn	Glu	Lys	Gly	Ile	Gly	Thr	Pro	Ser	Val	Ser	Ser	Ala	Leu	Val	Thr		
		610				615					620						

Thr Ser Lys Pro Ala Ala Gln Val Ala Leu Ser Asp Lys Asn Lys Met
 625 630 635 640
 Asp Met Ala Ile Ala Glu Lys Arg Leu Thr Ser Glu Gln Leu Ile Lys
 645 650 655
 Leu Glu Glu Val Lys Thr Ile Asn Ser Thr Ala Val Arg Leu Phe Trp
 660 665 670
 Lys Lys Arg Lys Leu Glu Glu Leu Ile Asp Gly Tyr Tyr Ile Lys Trp
 675 680 685
 Arg Gly Pro Pro Arg Thr Asn Asp Asn Gln Tyr Val Asn Val Thr Ser
 690 695 700
 Pro Ser Thr Glu Asn Tyr Val Val Ser Asn Leu Met Pro Phe Thr Asn
 705 710 715 720
 Tyr Glu Phe Phe Val Ile Pro Tyr His Ser Gly Val His Ser Ile His
 725 730 735
 Gly Ala Pro Ser Asn Ser Met Asp Val Leu Thr Ala Glu Ala Pro Pro
 740 745 750
 Ser Leu Pro Pro Glu Asp Val Arg Ile Arg Met Leu Asn Leu Thr Thr
 755 760 765
 Leu Arg Ile Ser Trp Lys Ala Pro Lys Ala Asp Gly Ile Asn Gly Ile
 770 775 780
 Leu Lys Gly Phe Gln Ile Val Ile Val Gly Gln Ala Pro Asn Asn Asn
 785 790 795 800
 Arg Asn Ile Thr Thr Asn Glu Arg Ala Ala Ser Val Thr Leu Phe His
 805 810 815
 Leu Val Thr Gly Met Thr Tyr Lys Ile Arg Val Ala Ala Arg Ser Asn
 820 825 830
 Gly Gly Val Gly Val Ser His Gly Thr Ser Glu Val Ile Met Asn Gln
 835 840 845
 Asp Thr Leu Glu Lys His Leu Ala Ala Gln Gln Glu Asn Glu Ser Phe
 850 855 860
 Leu Tyr Gly Leu Ile Asn Lys Ser His Val Pro Val Ile Val Ile Val
 865 870 875 880
 Ala Ile Leu Ile Ile Phe Val Val Ile Ile Ile Ala Tyr Cys Tyr Trp
 885 890 895
 Arg Asn Ser Arg Asn Ser Asp Gly Lys Asp Arg Ser Phe
 900 905

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